

FIG. 1

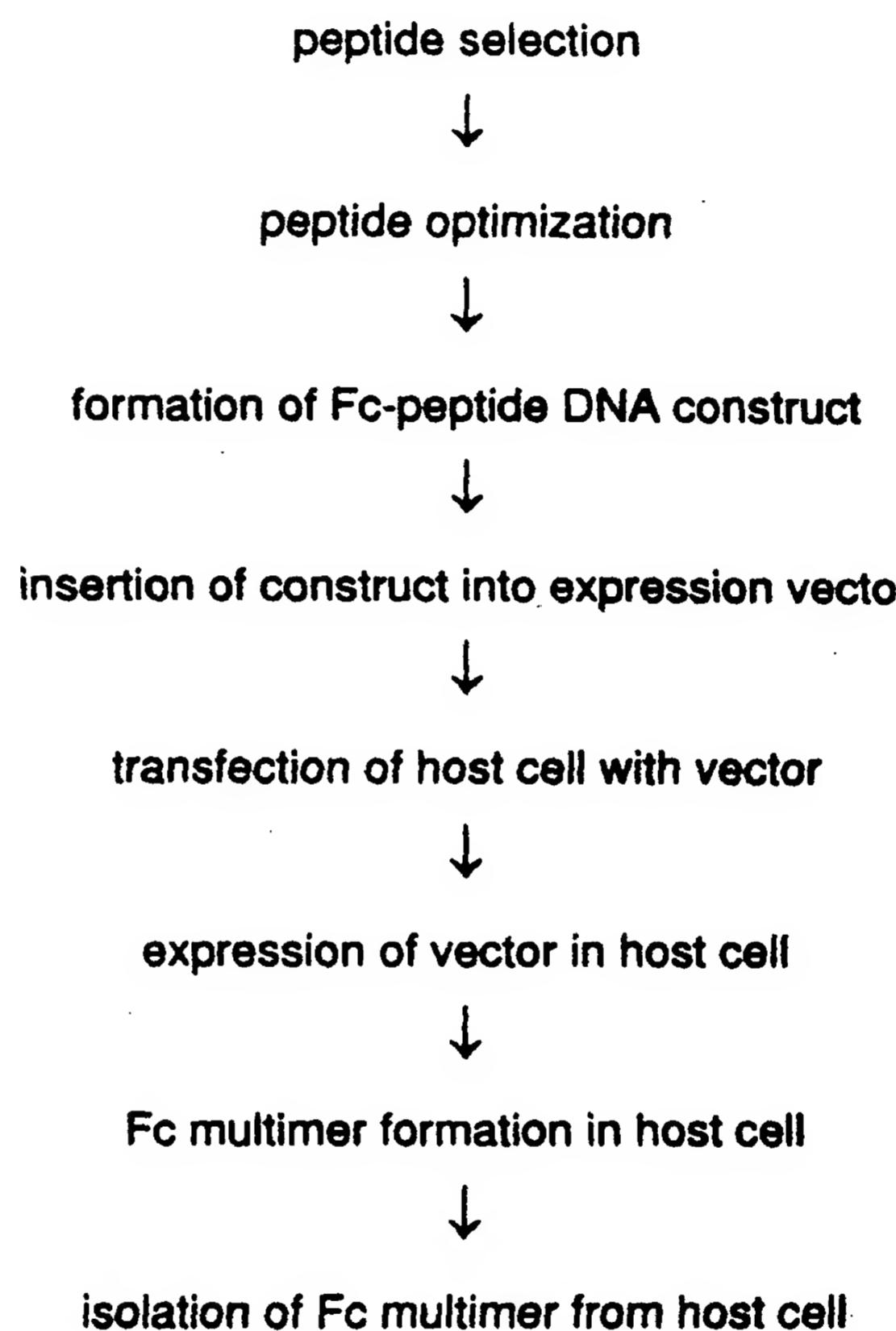


FIG. 2A

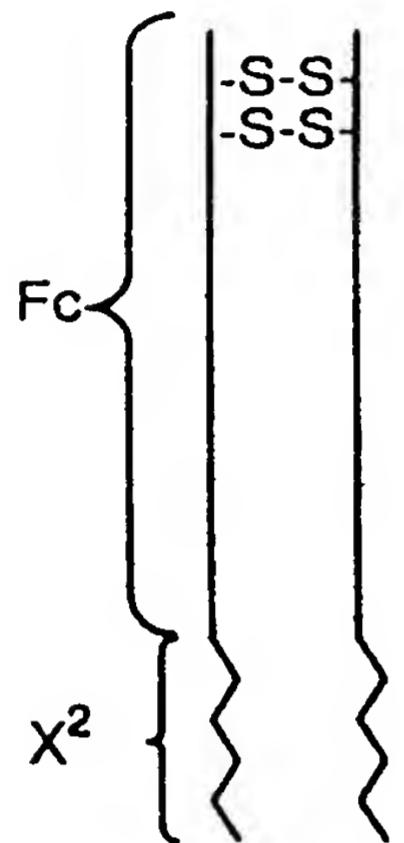


FIG. 2B

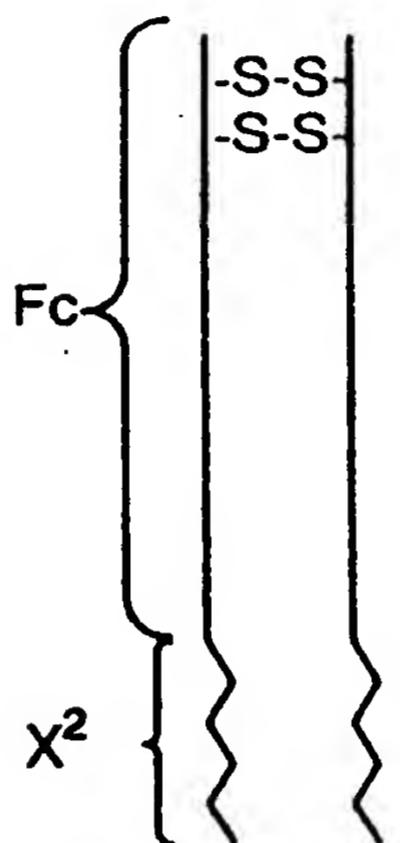


FIG. 2C

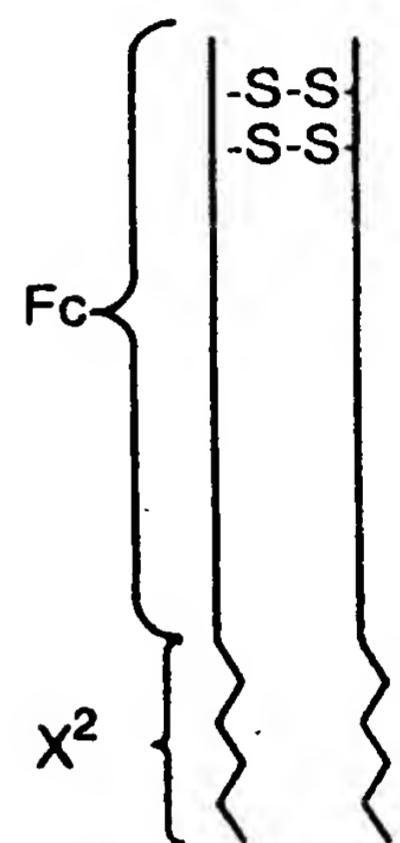


FIG. 2D

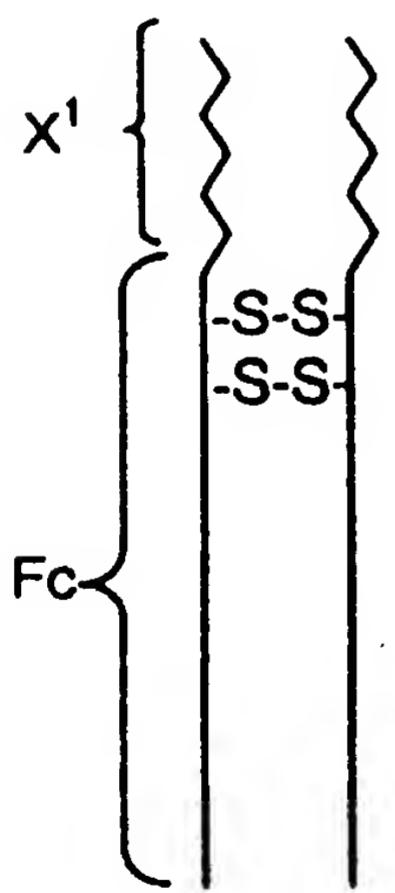


FIG. 2E

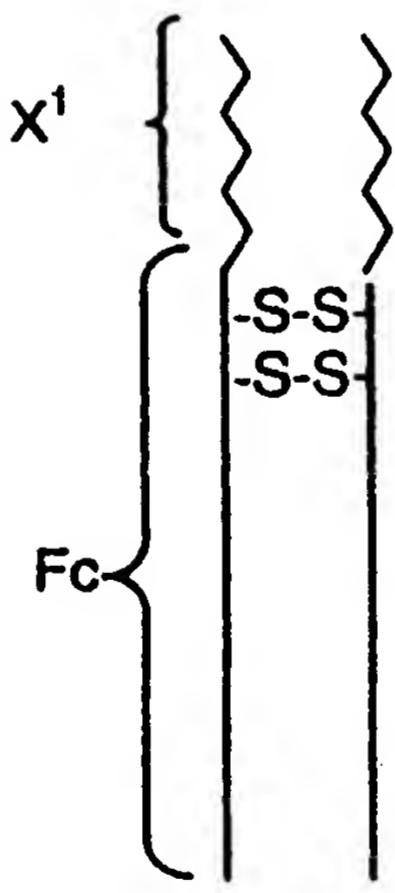


FIG. 2F

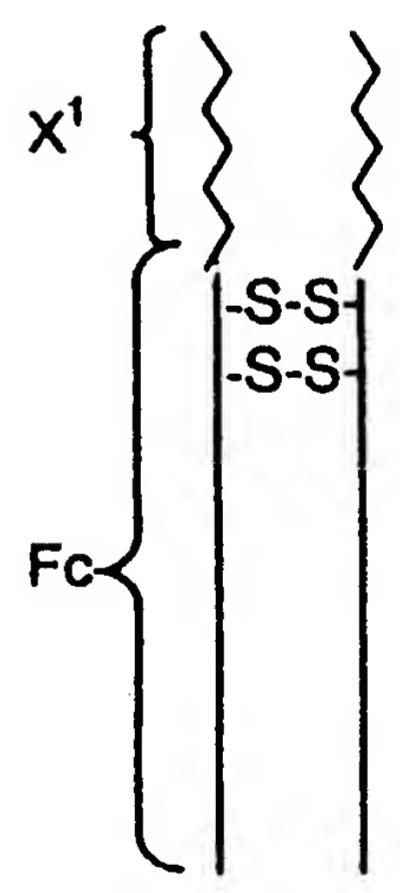


FIG. 3A

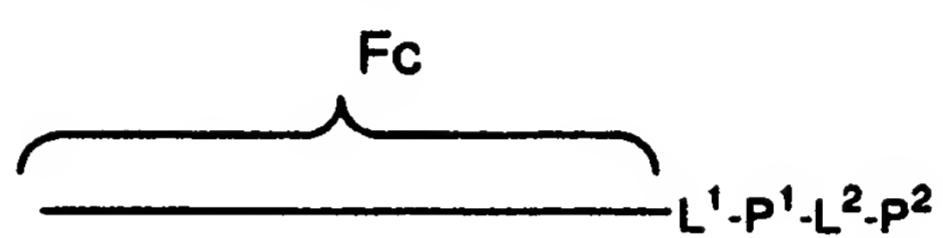


FIG. 3B

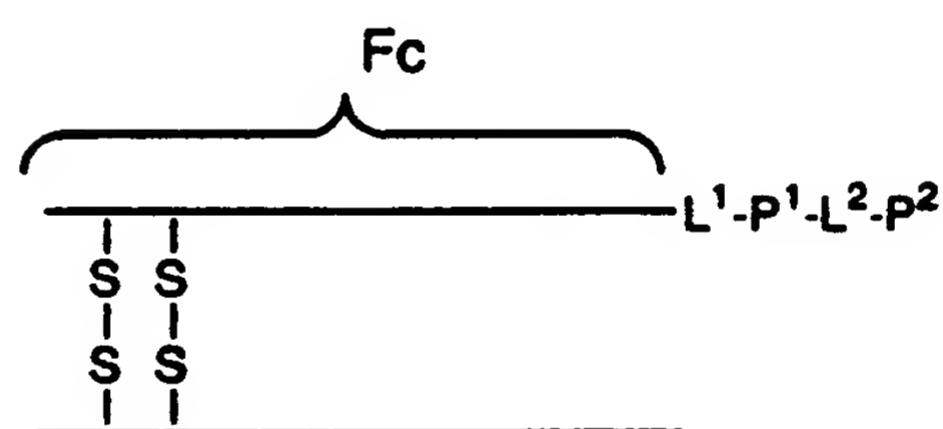


FIG. 3C

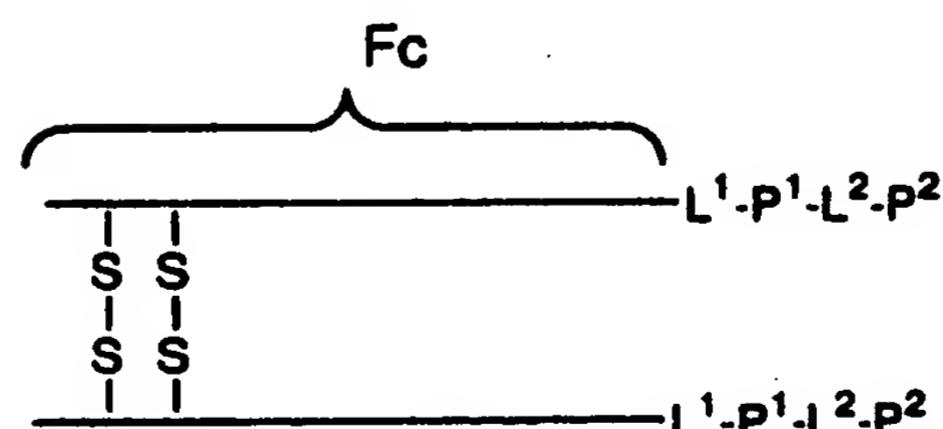


FIG. 4

ATGGACAAAACACATGTCCACCTGTCCAGCTCCGGAACTCCTGGGGGACCGTCA
 1 -----+-----+-----+-----+-----+-----+-----+-----+ 60
 TACCTGTTTGAGTGTACAGGTGAAACAGGTGAGGCCTTGAGGACCCCCCTGGCAGT

 a M D K T H T C P P C P A P E L L G G P S .

 GTCTTCCTCTTCCCCCAAAACCAAGGACACCCTCATGATCTCCGGACCCCTGAGGTC
 61 -----+-----+-----+-----+-----+-----+-----+-----+ 120
 CAGAAGGAGAAGGGGGTTTGGGTTCTGTGGAGTACTAGAGGCCTGGGACTCCAG

 a V F L F P P K P K D T L M I S R T P E V .

 ACATGCGTGGTGGACGTGAGCCACGAAGACCCCTGAGGTCAAGTTCAACTGGTACGTG
 121 -----+-----+-----+-----+-----+-----+-----+-----+ 180
 TGTACGCACCACCTGCACTCGGTGCTCTGGGACTCCAGTTCAAGTTGACCATGCAC

 a T C V V V D V S H E D P E V K F N W Y V .

 GACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGGGAGGAGCAGTACAACAGCACG
 181 -----+-----+-----+-----+-----+-----+-----+-----+ 240
 CTGCCGCACCTCCACGTATTACGGTCTGTTGGCGCCCTCCTCGTCATGTTGTCGTGC

 a D G V E V H N A K T K P R E E Q Y N S T .

 TACCGTGTGGTCAGCGTCCTCACCGTCTGCACCAGGACTGGCTGAATGGCAAGGAGTAC
 241 -----+-----+-----+-----+-----+-----+-----+-----+ 300
 ATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGCCTGACCGACTTACCGTTCTCATG

 a Y R V V S V L T V L H Q D W L N G K E Y .

 AAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCATCGAGAAAACCATCTCCAAAGCC
 301 -----+-----+-----+-----+-----+-----+-----+-----+ 360
 TTACGTTCCAGAGGTTGTTGGGAGGGTAGCTCTTGGTAGAGGTTTCGG

 a K C K V S N K A L P A P I E K T I S K A .

 AAAGGGCAGCCCCGAGAACACAGGTGTACACCCTGCCCATCCGGATGAGCTGACC
 361 -----+-----+-----+-----+-----+-----+-----+-----+ 420
 TTTCCCGTCGGGCTCTGGTCCACATGTGGACGGGGTAGGGCCCTACTCGACTGG

 a K G Q P R E P Q V Y T L P P S R D E L T .

 AAGAACCCAGGTCAAGCTGACCTGCCTGGTCAAAGGCTCTATCCCAGCGACATGCCGTG
 421 -----+-----+-----+-----+-----+-----+-----+-----+ 480
 TTCTTGGTCCAGTCGGACTGGACGGACCAGTTCCGAAGATAGGGTCGCTGTAGCGGCAC

 a K N Q V S L T C L V K G F Y P S D I A V .

 GAGTGGGAGAGCAATGGCAGCCGGAGAACAACTACAAGACCAACGCCCTCCGTGGAC
 481 -----+-----+-----+-----+-----+-----+-----+-----+ 540
 CTCACCCCTCTCGTTACCGTCCGGCTCTGTTGATGTTCTGGTGCAGGGCACGACCTG

 a E W E S N G Q P E N N Y K T T P P V L D .

 TCCGACGGCTCTTCTTCCCTACAGCAAGCTACCGTGGACAAGAGCAGGTGGCAGCAG
 541 -----+-----+-----+-----+-----+-----+-----+-----+ 600
 AGGCTGCCGAGGAAGAAGGAGATGTCGTTGAGTGGCACCTGTTCTCGTCCACCGTCGTC

 a S D G S F F L Y S K L T V D K S R W Q Q .

 GGGAACGTCTTCATGCTCCGTGATGCATGAGGCTCTGCACAAACCACTACACGCAGAAG
 601 -----+-----+-----+-----+-----+-----+-----+-----+ 660
 CCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTATGTGCGTCTTC

 a G N V F S C S V M H E A L H N H Y T Q K .

 AGCCTCTCCCTGTCTCCGGTAAA
 661 -----+-----+-----+-----+-----+-----+-----+-----+ 684
 TCGGAGAGGGACAGAGGCCCTTT

FIG. 5

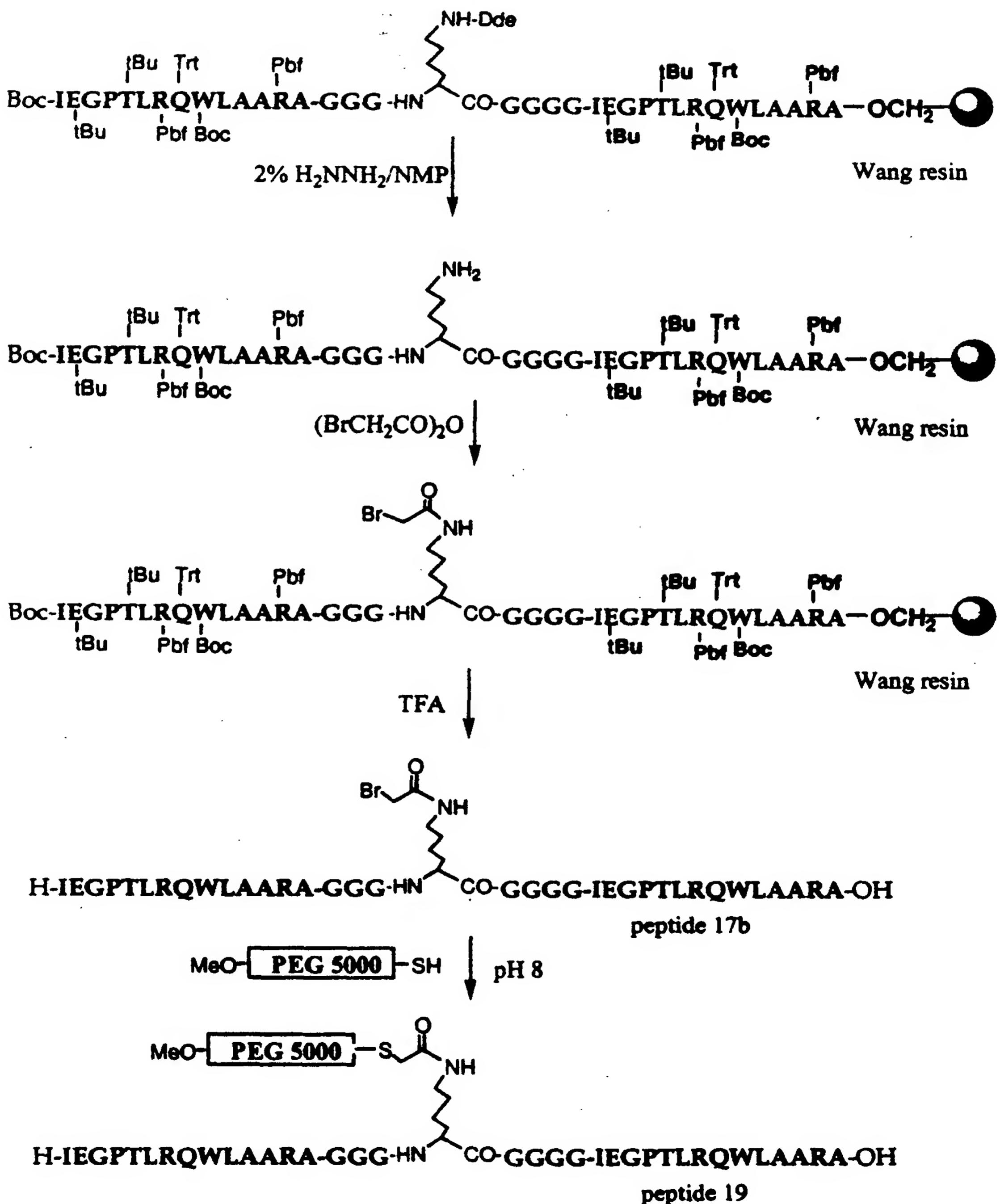


FIG. 6

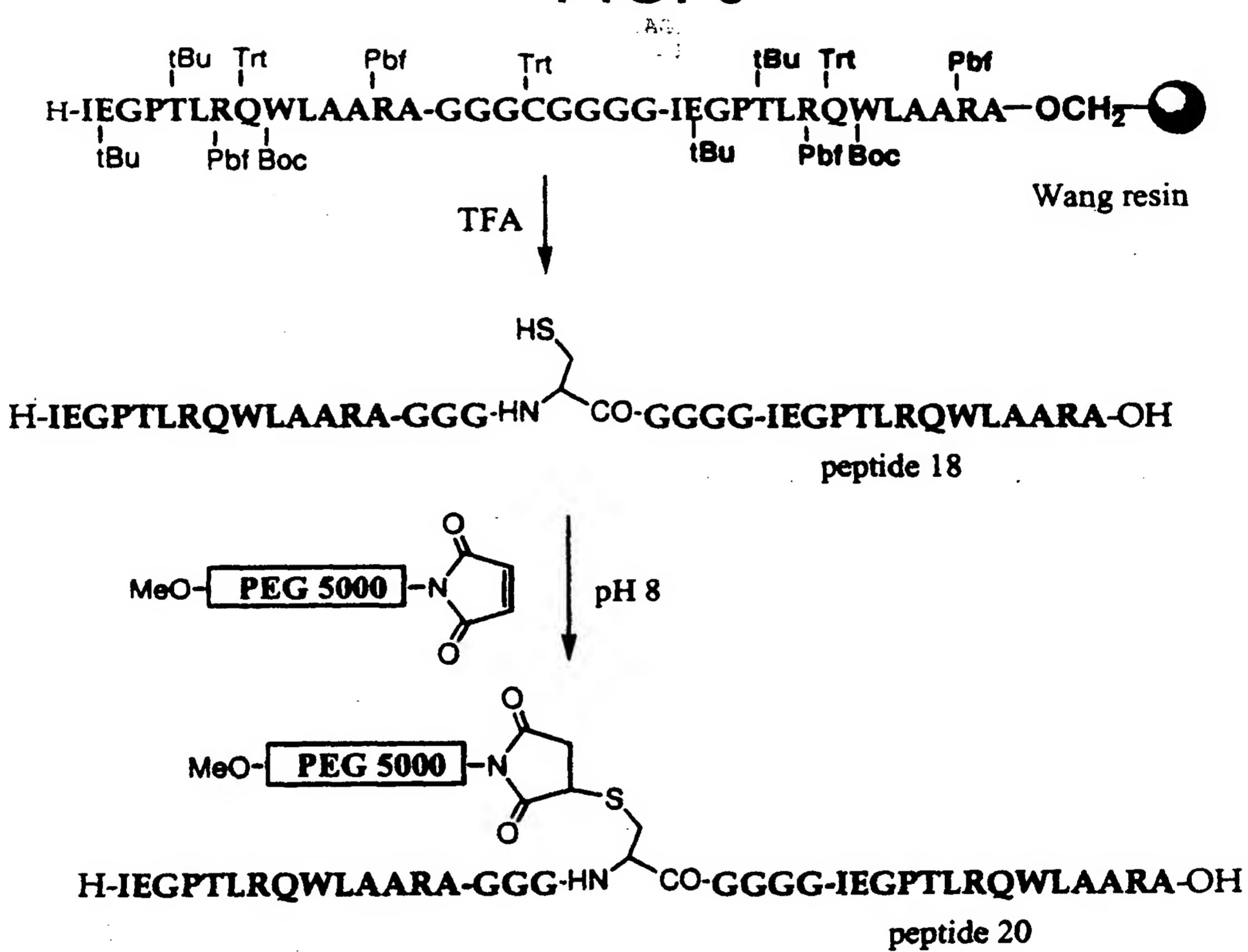


FIG. 7

XbaI
|
1 TCTAGATTTGTTTAACTAATTAAAGGAGGAATAACATATGGACAAAACACACATGTC 60
AGATCTAAACAAAATTGATTAATTCCCTCCTTATTGTATACCTGTTTGAGTGTGTACAG
M D K T H T C P -
c
61 CACCTTGTCCAGCTCCGGAACTCCTGGGGGACCGTCAGTCTTCCTCTTCCCCAAAAC 120
GTGGAACAGGTCGAGGCCTTGAGGACCCCCCTGGCAGTCAGAAGGAGAAGGGGGTTTG
P C P A P E L L G G P S V F L F P P K P -
c
121 CCAAGGACACCCATGATCTCCGGACCCCTGAGGTACATGCGTGGTGGACGTGA 180
GGTTCTGTGGGAGTACTAGAGGGCTGGGACTCCAGTGTACGCACCACCTGCACT
K D T L M I S R T P E V T C V V V D V S -
c
181 GCCACGAAGACCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATG 240
CGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACCTGCCGCACCTCCACGTATTAC
H E D P E V K F N W Y V D G V E V H N A -
c
241 CCAAGACAAAGCCGCGGGAGGAGCAGTACAACACGACGTACCGTGTGGTCAGCGTCCTCA 300
GGTTCTGTTCGGCGCCCTCCTCGTCATGTTGTCGTGCATGGCACACCAGTCGCAGGAGT
K T K P R E E Q Y N S T Y R V V S V L T -
c
301 CCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTCAAGGTCTCAAACAAAG 360
GGCAGGACGTGGTCTGACCGACTTACCGTTCTCATGTTCACGTTCCAGAGGTTGTTTC
V L H Q D W L N G K E Y K C K V S N K A -
c
361 CCCTCCCAGCCCCATCGAGAAAACCATCTCAAAGCCAAGGGCAGCCCCGAGAACAC 420
GGGAGGGTCGGGGTAGCTTTGGTAGAGGTTTCGGTTCCCGTCGGGCTTTGGT
L P A P I E K T I S K A K G Q P R E P Q -
c
421 AGGTGTACACCCCTGCCCATCCGGATGAGCTGACCAAGAACAGGTACGCCTGACCT 480
TCCACATGTGGGACGGGGTAGGGCCCTACTCGACTGGTTCTGGTCCAGTCGGACTGGA
V Y T L P P S R D E L T K N Q V S L T C -
c
481 GCCTGGTCAAAGGTTCTATCCAGCGACATGCCGTGGAGTGGAGAGCAATGGCAGC 540
CGGACCAAGTTCCGAAGATAGGGTCGCTGTAGCGGCACCTCACCCCTCGTTACCGTCG
L V K G F Y P S D I A V E W E S N G Q P -
c
541 CGGAGAACAACTACAAGACCAACGCCTCCGTGGACTCCGACGGCTCTTCTCCT 600
GCCTCTTGTGATGTTCTGGTGGAGGGCACGACCTGAGGCTGCCAGGAAGAAGGAGA
E N N Y K T T P P V L D S D G S F F L Y -
c
601 ACAGCAAGCTACCGTGGACAAGAGCAGGTGGCAGCAGGGAACGTCTCTCATGCTCCG 660
TGTGTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTCCCCCTGCAGAACAGTACGAGGC
S K L T V D K S R W Q Q G N V F S C S V -
c
661 TGATGCATGAGGCTCTGCACAACCACTACACGCAGAACAGGCTCTCCCTGTCTCCGGTA 720
ACTACGTACTCCGAGACGTGGATGTGGCTCTCGGAGAGGGACAGAGGCCAT
M H E A L H N H Y T Q K S L S L S P G K -
c
721 AAGGTGGAGGTGGTGGTATCGAAGGTCCGACTCTCGCTCAGTGGCTGGCTGCTCGTGC 780
TTCCACCTCCACCAACCATAGCTCCAGGCTGAGACGCAGTCACCGACCGACGACGAA
G G G G G I E G P T L R Q W L A A R A * -
c
BamHI
|
781 AATCTCGAGGATCC 794
TTAGAGCTCCTAGG

FIG. 8

XbaI

TCTAGATTGTTTAACTAATTAAAGGAGGAATAACATATGGACAAAACCTCACACATGTC
1+.....+.....+.....+.....+.....+.....+.....+.....+.....+ 60
AGATCTAACAAAATTGATTAATTCCCTCCTTATTGTATACCTGTTTGAGTGTGTACAG
M D K T H T C P

c

61 CACCTTGTCCAGCTCCGGAACTCCTGGGGGACCGTCAGTCTCCTCTTCCCCCAAAAC
GTGGAACAGGTCGAGGCCTTGAGGACCCCCCTGGCAGTCAGAAGGAGAAGGGGGTTTG
c P C P A P E L L G G P S V F L F P P K P

121 CCAAGGACACCCTCATGATCTCCGGACCCCTGAGGTACATGCGTGGTGGACGTGA
GGTCCTGTGGGAGTACTAGAGGGCCTGGGACTCCAGTGTACGCACCACCTGCACT
c K D T L M I S R T P E V T C V V V D V S

181 GCCACCGAAGACCCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATG
CGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACCTGCCACCTCACGTATTAC
c H E D P E V K F N W Y V D G V E V H N A

241 CCAAGACAAAGCCGGGGAGGAGCAGTACAACACAGCACGTACCGTGTGGTCAGCGTCTCA
GGTCCTGTTCGCGCCCTCTCGTCATGTTGTCGTGCATGGCACACCAGTCGCAGGAGT
c K T K P R E E Q Y N S T Y R V V S V L T

301 CCGTCCTGCACCAGGACTGGCTGAATGCAAGGAGTACAAGTGCAGGTCTCCAAACAAAG
GGCAGGGACGTGGCCTGACCGACTTACCGTTCTCATGTCACGTTCCAGAGGTTGTTTC
c V L H Q D W L N G K E Y K C K V S N K A

361 CCCTCCCAGCCCCATCGAGAAAACCATCTCAAAGCCAAGGGCAGCCCCGAGAACAC
GGGAGGGTCGGGGTAGCTCTTGGTAGAGGTTCGGTTCCCGTCGGGCTCTGGTG
c L P A P I E K T I S K A K G Q P R E P Q

421 AGGTGTACACCCCTGCCCATCCGGATGAGCTGACCAAGAACAGGTACGCTGACCT
TCCACATGTGGGACGGGGTAGGGCCCTACTCGACTGGTCTTGGTCCAGTCGGACTGGA
c V Y T L P P S R D E L T K N Q V S L T C

481 GCCTGGTCAAAGGTTCTATCCAGCGACATGCCGTGGAGTGGAGAGCAATGGGCAGC
CGGACCAGTTCCGAAGATAGGGTCGCTGTAGCGGCACCTCACCCCTCGTTACCGTCG
c L V K G P Y P S D I A V E W E S N G Q P

541 CGGAGAACAACTACAAGACCAACGCCCTCCGTGCTGGACTCCGACGGCTCCCTTCTCT
GCCTCTTGTGATGTTCTGGTGGAGGGCACGACCTGAGGCTGCCGAGGAAGAAGGAGA
c E N N Y K T T P P V L D S D G S P F L Y

601 ACAGCAAGCTACCGTGGACAAGAGCAGGTGGAGCAGGGAACGTCTCTCATGCTCCG
TGTGTTGAGTGGCACCTGTTCTGTCACCGTCGTCCCTGAGAAGAGTACGAGGC
c S K L T V D K S R W Q Q G N V F S C S V

661 TGATGCATGAGGCTCTGCACAAACACTACACGAGAAGAGCCTCTCCCTGTCTCCGGTA
ACTACGTACTCCGAGACGTGTTGGTAGTGTGCGTCTCTCGGAGAGGGACAGAGGCCAT
c M H E A L H N H Y T Q K S L S L S P G K

721 AAGGTGGAGGTGGTGGTATCGAAGGTCCGACTCTGCGTCAGTGGCTGGCTGCTGCTG
TTCCACCTCCACCACCATAGCTTCCAGGCTGAGACGCAGTCACCGACCGAGCACGAC
c G G G G G I E G P T L R Q W L A A R A G

781 GTGGTGGAGGTGGCGGGAGGTATTGAGGGCCAACCCCTGCCAATGGCTTGAGCAC
CACCAACCTCCACCGCCGCTCCATAACTCCGGTTGGAGCGGTTACCGAACGTGCTG
c G G G G G G I E G P T L R Q W L A A R

BamHI

841 GCGCATTAATCTCGAGGATCCG
CGCGTATTAGAGCTCTAGGC

FIG. 9

XbaI

1 TCTAGATTGTTTAACATAATTAAAGGAGGAATAACATATGATCGAAGGTCCGACTCTGC
1 60 AGATCTAAACAAAATTGATTAATTCTCCTTATTGTATACTAGCTTCAGGCTGAGACG
c M I E G P T L R .
61 GTCAGTGGCTGGCTGCTCGTGCCTGGCGGTGGCGGAGGGGGTGGCATTGAGGGCCAA
c 120 CAGTCACCGACCGACGGAGCACCGCCACCACCGCCTCCCCCACCGTAACCTCCGGGTT
c Q W L A A R A G G G G G G G G I E G P T .
121 CCCTTCGCCAATGGCTTGCAGCACGCCAGGGGGAGGGCGGTGGGACAAAACACAT
c 180 GGGAAAGCGGTTACCGAACGTCGTGCCTGGCTCCCCCTCCGCCACCCCTGTTTGAGTGTGTA
c L R Q W L A A R A G G G G G D K T H T C .
181 GTCCACCTTGCCTGCCAGCACCTGAACTCCTGGGGGACCGTCAGTTCTCTTCCCCCAA
c 240 CAGGTGGAACGGGTCTGGACTTGAGGACCCCCCTGGCAGTCAAAAGGAGAAGGGGGTT
c P P C P A P E L L G G P S V F L F P P K .
241 AACCCAAGGACACCCCTCATGATCTCCGGACCCCTGAGGTACATGCGTGGTGGGACG
c 300 TTGGGTTCTGTGGGAGTACTAGAGGGCCTGGGACTCCAGTGTACGCACCAACCTGC
c P K D T L M I S R T P E V T C V V V D V .
301 TGAGCCACGAAGACCCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATA
c 360 ACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACCTGCCACCTCCACGTAT
c S H E D F R V K F N W Y V D G V E V H N .
361 ATGCCAAGACAAAGCCGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCC
c 420 TACGGTTCTGTTCGCGCCCTCCTCGTCATGTTGTGCATGGCACACCAGTCGCAGG
c A K T K P R E E Q Y N S T Y R V V S V L .
421 TCACCGTCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAGGTCTCCAACA
c 480 AGTGGCAGGACGTGGCCTGACCGACTTACCGTTCTCATGTTCACGTTCCAGAGGTTGT
c T V L H Q D W L N G K E Y K C K V S N K .
481 AAGCCCTCCCAGCCCCATCGAGAAAACCATCTCAAAGCCAAGGGCAGCCCCGAGAAC
c 540 TTCGGGAGGGTCGGGGTAGCTCTTGGTAGAGGTTCGGTTCCCGTCGGGCTCTG
c A L P A P I E K T I S K A K G Q P R E P .
541 CACAGGTGTACACCCCTGCCCCATCCCGGGATGAGCTGACCAAGAACCAAGGTCAAGCCTGA
c 600 GTGTCCACATGTGGACGGGGTAGGGCCCTACTCGACTGGTTCTGGTCCAGTCGGACT
c Q V Y T L P P S R D E L T K N Q V S L T .
601 CCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATGCCGTGGAGTGGAGAGCAATGGC
c 660 GGACGGACCAGTTCCGAAGATAGGGTCGCTGAGCGCACCTCACCTCTCGTTACCCG
c C L V K G F Y P S D I A V E W E S N G Q .
661 AGCCGGAGAACAACTACAAGACCAACGCCCTCCGTGGACTCCGACGGCTCTTCTTCC
c 720 TCGGCCTCTGTTGATGTTCTGGTGCCTGGAGGGCACGACCTGAGGCTGCCAGGAAGAAGG
c P E N N Y K T T P P V L D S D G S F P L .
721 TCTACAGCAAGCTACCGTGGACAAGAGCAGGTGGCAGCAGGGAACGTCTCTCATGCT
c 780 AGATGTCGTTGAGTGGCACCTGTTCTCGTCCACCGTCGTCCCTGAGAAGAGTACGA
c Y S K L T V D K S R W Q Q G N V F S C S .
781 CCGTGATGCATGAGGCTCTGCACAACCAACTACACGCAGAAGAGCCTCTCCCTGTCTCCGG
c 840 GGCACACTACGTACTCCGAGACGTGTTGGTATGTCGCTCTCGGAGAGGGACAGAGGCC
c V M H E A L H N H Y T Q K S L S L S P G .
BamHI
1 GTAAATAATGGATCC
841 855
c CATTATTACCTAGG
c K *

FIG. 10

XbaI

1 TCTAGATTGTTAACTAATTAAAGGAGGAATAACATATGATCGAAGGTCCGACTCTGC
c AGATCTAAACAAAATTGATTAATTCCCTCCTATTGTATACTAGCTTCCAGGCTGAGACG
M I E G P T L R
61 GTCAGTGGCTGGCTGCTCGTGGCTGGAGGCCGTGGGACAAAACACACATGTCCAC
c CAGTCACCGACCGACGACGACCACTCCGCCACCCCTGTTTGAGTGTACAGGTG
Q W L A A R A G G G G D K T H T C P P
121 CTTGCCACGACCTGAACCTGGGGGACCGTCAGTTCCCTCTCCCCCAAAACCA
c GAACGGGTGGACTTGAGGACCCCCCTGGCAGTCAAAGGAGAAGGGGGTTTGGGT
C P A P E L L G G P S V F L F P P K P K
181 AGGACACCCCTCATGATCTCCGGACCCCTGAGGTACATGCGTGGTGGACGTGAGCC
c TCCTGTGGGAGTACTAGAGGGCTGGGACTCCAGTGTACCCACCCACCTGCACTCGG
D T L M I S R T P E V T C V V V D V S H
241 ACGAAGACCCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCA
c TGCTTCTGGACTCCAGTTCAAGTTGACCATGCACCTGCCACCTCACGTATTACGGT
E D P E V K F N W Y V D G V E V H N A K
301 AGACAAAGCCGGAGGAGCAGTACAACACGACGTACCGTGTGGTCAGCGTCCTCACCG
c TCTGTTTGGCGCCCTCCTCGTCATGTTGTGTCATGGCACACCAGTCGCAAGGAGTGGC
T K P R E E Q Y N S T Y R V V S V L T V
361 TCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAGGTCTCCAACAAAGCC
c AGGACGTGGTCCTGACCGACTTACCGTTCTCATGTTCACGTTCCAGAGGTTTTGGG
L H Q D W L N G K E Y K C K V S N K A L
421 TCCCAGCCCCATCGAGAAAACCATCTCAAAGCCAAAGGGCAGCCCCGAGAACACAGG
c AGGGTCGGGGTAGCTCTTGGTAGAGGTTTCGGTTCCCGTCGGGCTCTGGTGTCC
P A P I E K T I S K A K G Q P R E P Q V
481 TGTACACCCCTGCCCCATCCGGATGAGCTGACCAAGAACAGGTCAAGCTGACCTGCC
c ACATGTGGACGGGGTAGGGCCCTACTCGACTGGTTCTGGTCCAGTCGGACTGGACGG
Y T L P P S R D E L T K N Q V S L T C L
541 TGGTCAAAGGTTCTATCCCAGCGACATGCCGTGGAGTGGAGAGCAATGGCAGCCGG
c ACCAGTTCCGAAGATAGGGTCGCTGTAGCGGCACCTCACCTCTCGTTACCCGTGGCC
V K G F Y P S D I A V E W E S N G Q P E
601 AGAACAACTACAAGACCACGCCCTCCGTGGACTCCGACGGCTCCTTCTCTACA
c TCTTGTGATGTTCTGGTGGAGGGCACGACCTGAGGCTGCCAGGAAGAAGGAGATGT
N N Y K T T P P V L D S D G S F F L Y S
661 GCAAGCTACCGTGGACAAGAGCAGGTGGCAGCAGGGAACGTCTCTCATGCTCCGTGA
c CGTCGAGTGGCACCTGTTCTCGTCACCGTCGTCCCCCTGCAGAAGAGTACGAGGCAGT
K L T V D K S R W Q Q G N V F S C S V M
721 TGCATGAGGCTCTGCACAACACTACACGAGAAGAGCCTCTCCCTGTCTCCGGTAAAT
c ACGTACTCCGAGACGTGGTGTGATGTGCGTCTCTCGGAGAGGGACAGAGGCCATTAA
H E A L H N H Y T Q K S L S L S P G K *
781 AATGGATCC
TTACCTAGG 789

FIG.11

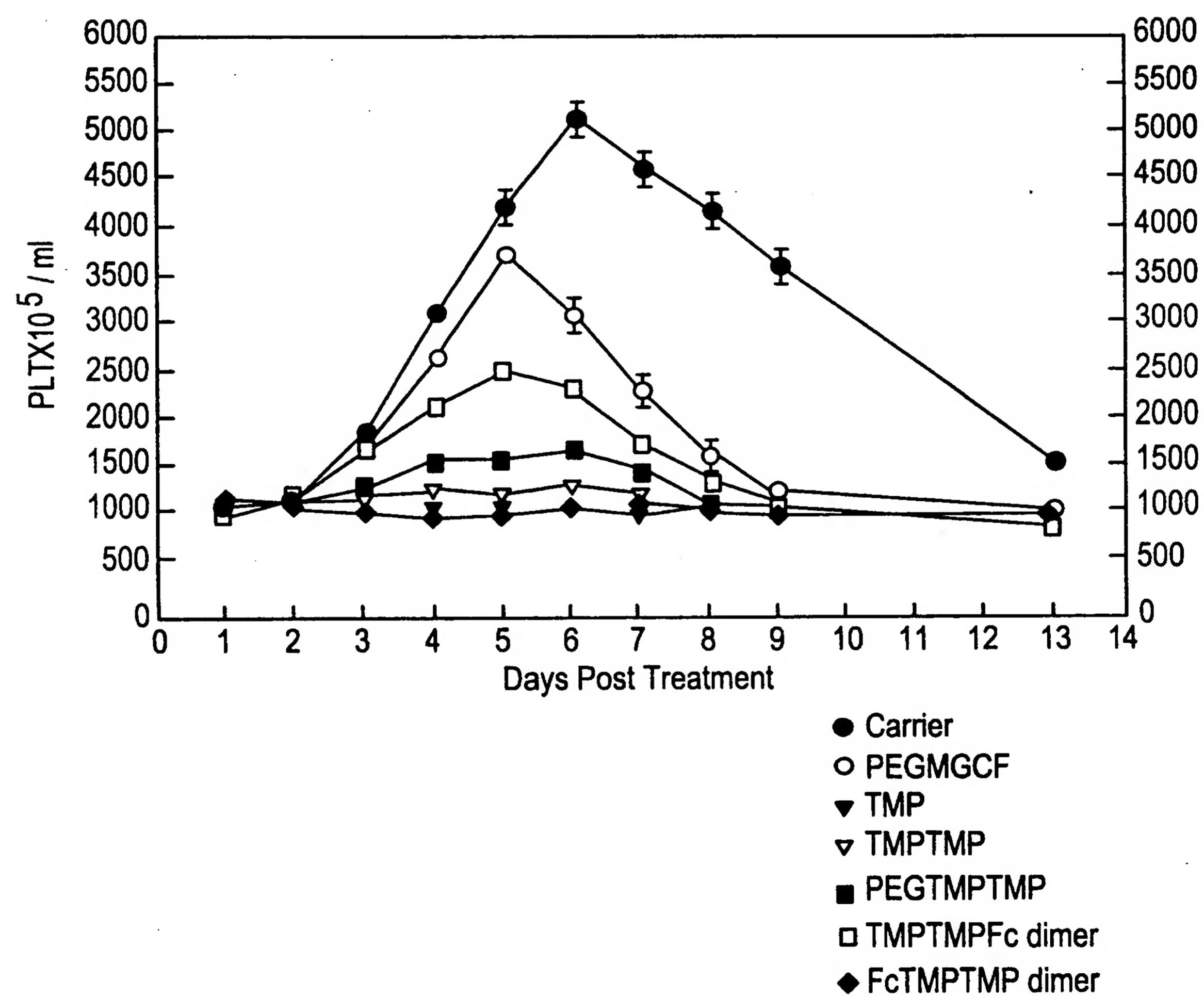


FIG.12

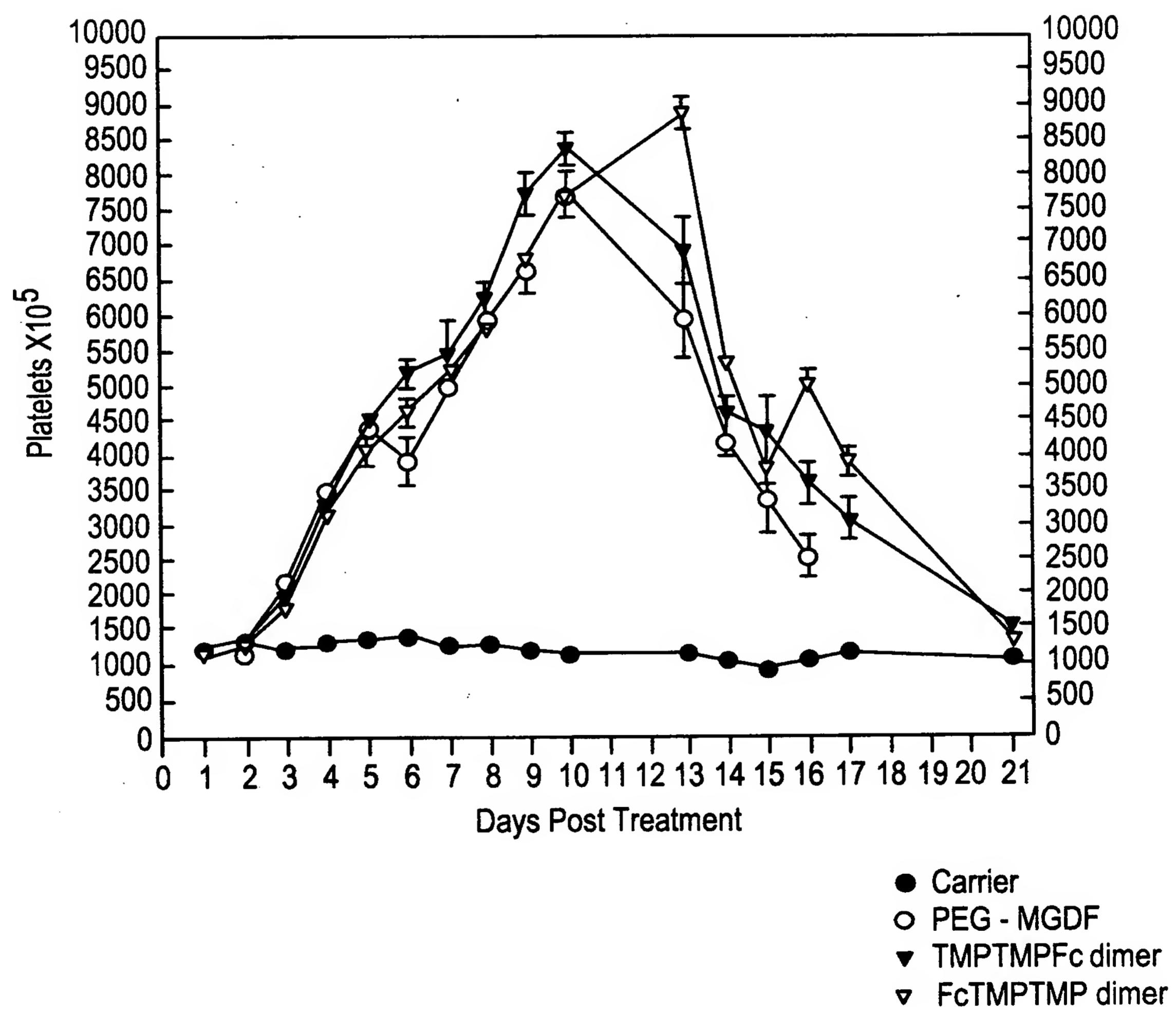


FIG. 13

XbaI

1 TCTAGATTGTTAACTAATTAAAGGAGGAATAACATATGGACAAACTCACACATGTC 60
1 AGATCTAAACAAAATTGATTAATTCTCCTTATTGTATACCTGTTGAGTGTGTACAG
c M D K T H T C P -
61 CACCTTGTCCAGCTCCGGAACTCCTGGGGGACCGTCAGTCTCCTCTCCCCAAAAC 120
c GTGGAACAGGTCGAGGCCTTGAGGACCCCCCTGGCAGTCAGAAGGGAGAAGGGGGTTTG
c P C P A P E L L G G P S V F L F P P K P -
121 CCAAGGACACCCCTCATGATCTCCGGACCCCTGAGGTACATGCCTGGTGGACGTGA 180
c GGTTCTGTGGAGTACTAGAGGCCTGGGACTCCAGTGTACGCACCACCTGCACT
c K D T L M I S R T P E V T C V V V D V S -
181 GCCACGAAGACCCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATG 240
c CGGTGCTCTGGACTCCAGTTCAAGTTGACCATGCACCTGCCGCACCTCACGTATTAC
c H E D P E V K F N W Y V D G V E V H N A -
241 CCAAGACAAAGCCGGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCA 300
c GGTTCTGTTCGGCGCCCTCTCGTCATGTTGTCATGGCACACCAGTCGCAGGAGT
c K T K P R E E Q Y N S T Y R V V S V L T -
301 CCGTCCTGCACCAAGGACTGGCTGAATGGCAAGGAGTACAAGTCAAGGTCTCAACAAAG 360
c GGCAGGACGTGGTCTGACCGACTTACCGTTCTCATGTTCACGTTCCAGAGGTTGTTTC
c V L H Q D W L N G K E Y K C K V S N K A -
361 CCCTCCCAGCCCCATCGAGAAAACCATCTCAAAGCAAAGGGCAGCCCCGAGAACAC 420
c GGGAGGGTCGGGGTAGCTCTTGTAGAGGTTCGGTTCCCGTCCGGCTCTGGTG
c L P A P I E K T I S K A K G Q P R E P Q -
421 AGGTGTACACCCCTGCCCATCCGGATGAGCTGACCAAGAACCAAGGTCAAGCTGACCT 480
c TCCACATGTGGACGGGGTAGGGCCCTACTCGACTGGTTCTGGTCCAGTCGGACTGGA
c V Y T L P P S R D E L T K N Q V S L T C -
481 GCCTGGTCAAAGGTTCTATCCCAGCGACATGCCGTGGAGGAGCAATGGCAGC 540
c CGGACCAAGTTCCGAAGATAGGGTCGTGTACCGGCACCTCACCCCTCTCGTTACCGTCG
c L V K G F Y P S D I A V E W E S N G Q P -
541 CGGAGAACAACTACAAGACCAAGCCCTCCCGTGGACTCCGACGGCTCTTCTCCT 600
c GCCTCTTGTGATGTTCTGGTGGAGGGACGACCTGAGGCTGCCAGGAAGAAGGAGA
c E N N Y K T T P P V L D S D G S F F L Y -
601 ACAGCAAGCTACCGTGGACAAGAGCAGGTGGCAGCAGGGAACGTCTCATGCTCCG 660
c TGTGTTCGAGTGGCACCTGTTCTCGTCACCGTCGTCCCTGAGAAGAGTACGAGGC
c S K L T V D K S R W Q Q G N V F S C S V -
661 TGATGCATGAGGCTCTGCACAACCACTACACGAGAAGAGCCTCTCCCTGTCTCCGGTA 720
c ACTACGTACTCCGAGACGTGTTGGTGTAGTGCCTCTCGGAGAGGGACAGAGGCCAT
c M H E A L H N H Y T Q K S L S L S P G K -
721 AAGGTGGAGGTGGTGGAGGTACTTACTCTTGCCACTTCGGCCCGCTGACTTGGGTTT 780
c TTCCACCTCCACCAACCTCCATGAATGAGAACGGTGAAGCCGGGACTGAACCCAAA
c G G G G G G G T Y S C H F G P L T W V C -
BamHI
|
781 GCAAACCGCAGGGTGGTTAAATCTCGTGGATCC 812
c CGTTTGGCGTCCCACCAATTAGAGCACCTAGG
c K P Q G G *

FIG. 14

XbaI

1 TCTAGATTGTTAACTAATTAAAGGAGGAATAACATATGGGAGGTACTTACTCTTGC 60
1 AGATCTAAACAAAATTGATTAATTCTCTCTTATTGTATACCCCTCCATGAATGAGAACGG
c M G G T Y S C H -

61 ACTTCGGCCCGCTGACTTGGGTATGTAAGCCACAAGGGGTGGGGAGGGGGGGGACA 120
61 TGAAGCCGGCGACTGAACCCATACATTGGTGTCCCCCACCCCTCCGCCCCCTGT
c F G P L T W V C K P Q G G G G G G G D K -

121 AAACTCACACATGTCCACCTGCCAGCACCTGAACCTGGGGGACCGTCAGTTTCC 180
121 TTTGAGTGTGTACAGGTGGAACGGGTGGACTTGAGGACCCCCCTGGCAGTCAAAAGG
c T H T C P P C P A P E L L G G P S V F L -

181 TCTTCCCCAAAACCAAGGACACCCCTCATGATCTCCGGACCCCTGAGGTACATGCG 240
181 AGAAGGGGGTTTGGGTTCTGTGGAGTACTAGAGGGCTGGGACTCCAGTGTACGC
c F P P K P K D T L M I S R T P E V T C V -

241 TGGTGGTGGACGTGAGCCACGAAGACCCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCG 300
241 ACCACCAACCTGCACTCGGTGCTCTGGACTCCAGTTCAAGTTGACCATGCACCTGCCGC
c V V D V S H E D P E V K F N W Y V D G V -

301 TGGAGGTGCATAATGCCAAGACAAAGCCGGAGGAGCAGTACAACACGTACCGTG 360
301 ACCTCCACGTATTACGGTTCTGTTGGCGCCCTCTCGTCAAGTTGACCATGGCAC
c E V H N A K T K P R E E Q Y N S T Y R V -

361 TGGTCAGCGTCCTCACCGTCCTGCACCAAGGACTGGCTGAATGCAAGGAGTACAAGTGC 420
361 ACCAGTCGCAAGGAGTGGCAGGACGTGGCCTGACCGACTTACCGTTCTCATGTTACGT
c V S V L T V L H Q D W L N G K E Y K C K -

421 AGGTCTCAAACAAAGCCCTCCAGCCCCATCGAGAAAACCATCTCAAAGCAAAGGGC 480
421 TCCAGAGGTTGGGGAGGGTCGGGGTAGCTCTGGTAGAGGTTGGGGTTCCCG
c V S N K A L P A P I E K T I S K A K G Q -

481 AGCCCCGAGAACACAGGTGTACACCCCTGCCCATCCGGATGAGCTGACCAAGAAC 540
481 TCGGGGCTCTGGTGTCCACATGTGGGACGGGGTAGGGCCCTACTCGACTGGTTCTTGG
c P R E P Q V Y T L P P S R D E L T K N Q -

541 AGGTCAAGCCTGACCTGCCTGGTCAAAGGCTCTATCCAGCGACATGCCGTGGAGTGG 600
541 TCCAGTCGGACTGGACGGACCAGTTCCGAAGATAGGGTCGCTGTAGCGGCACCTCACCC
c V S L T C L V K G F Y P S D I A V B W E -

601 AGAGCAATGGGAGCCGGAGAACAACTACAAGACCAAGCCCTCCGTGCTGGACTCCGACG 660
601 TCTCGTTACCCGTGGCCTCTTGTGATGTTCTGGTGGAGGGCACGACCTGAGGCTGC
c S N G Q P E N N Y K T T P P V L D S D G -

661 GCTCCTTCTCCTCTACAGCAAGCTACCGTGGACAAGAGCAGGTGGCAGCAGGGAAACG 720
661 CGAGGAAGAAGGAGATGTCGTTGAGTGGCACCTGTTCTCGTCCACCGTCGTCCCCCTG
c S F P L Y S K L T V D K S R W Q Q G N V -

721 TCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAAACCACTACACGAGAACCTCT 780
721 AGAAGAGTACGAGGCACCTACGTACTCCGAGACGTGTTGGTGTGCGTCTTCGGAGA
c F S C S V M H E A L H N H Y T Q K S L S -

BamHI

781 CCCTGTCTCCGGTAAATAATGGATCC 807
781 GGGACAGAGGCCATTATACCTAGG
c L S P G K *

FIG. 15

XbaI

1 TCTAGATTTGAGTTAACTTTAGAAGGAGGAATAAAATATGGAGGTACTTACTCTTG 60
b AGATCTAAACTCAAAATTGAAAATCTCCTCCTTATTTATACCCCTCCATGAATGAGAAC
M G G T Y S C -
61 CCACTTGGCCCAC TGACTTGGTTGCAAACCGCAAGGTGGCGCGCGCGGTGG 120
b GGTGAAGCCGGGTGACTGAACCCAAACGTTGGCGTCCCACCGCCGCCGCCACC
H F G P L T W V C K P Q G G G G G G G G -
121 TACCTATTCTGTCA TTTGGCCCGCTGACCTGGTATGTAAGCCACAAGGGGTGGGG 180
b ATGGATAAGGACAGTAAAACCGGGGACTGGACCCATACATTGGTGTCCCCACCCCC
T Y S C H F G P L T W V C K P Q G G G G G G -
181 AGGCCGGGGGGACAAA ACTCACACATGTCCACCTGCCAGCACCTGAACCTGGGGGG 240
b TCCGCCCCCTGTTGAGTGTGTACAGGTGGAACGGTCGTGGACTTGAGGACCCCC
G G G D K T H T C P P C P A P E L L G G -
241 ACCGTCA GTTTCTCTCCCAAAACCAAGGACACCCATGATCTCCGGACCCC 300
b TGGCAGTCAAAGGAGAAGGGGGTTTGGGTCCTGTGGAGTACTAGAGGGCTGGGG
P S V F L P P P K P K D T L M I S R T P -
301 TGAGGTCA CATGCGTGGTGGACGTGAGCCACGAAGACCCCTGAGGTCAAGTCAACTG 360
b ACTCCAGTGTACGCACCACCACTGCACTCGTGCTCTGGACTCCAGTCAAGTGA
E V T C V V V D V S H E D P E V K F N W -
361 GTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGGGGAGGAGCAGTACAA 420
b CATGCACCTGCCGCACCTCCACGTATTACGGTCTGTTGGCCCTCCGTCACTGTT
Y V D G V E V H N A K T K P R E Q Y N -
421 CAGCACGTACCGTGTGGTCAGCGTCTCACCGTCTGCACCAAGGACTGGCTGAATGGCAA 480
b GTCGTGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGCCTGACCGACTACCGTT
S T Y R V V S V L T V L H Q D W L N G K -
481 GGAGTACAAGTCAAGGTCTCAACAAAGCCCTCCCAGCCCCATCGAGAAAACCATCTC 540
b CCTCATGTTACGTTCCAGAGGTTGTTGGAGGGTAGCTCTTGGTAGAG
E Y K C K V S N K A L P A P I E K T I S -
541 CAAAGCAAAGGGCAGCCCCGAGAACCAACAGGTGTACACCCCTGCCCATCCGGGATGA 600
b GTTTCGGTTCCCGTCGGGCTCTGGTGTCCACATGTGGACGGGGTAGGGCCCTACT
K A K G Q P R E P Q V Y T L P P S R D E -
601 GCTGACCAAGAACCAAGGTCAGCCTGACCTGCCTGGTCAAAGGTTCTATCCAGCGACAT 660
b CGACTGGTCTGGTCCAGTCGGACTGGACGGACCAGTTCCGAAGATAGGGTCGCTGTA
L T K N Q V S L T C L V K G F Y P S D I -
661 CGCCGTGGAGTGGAGAGCAATGGCAGCCGGAGAACAACTACAAGACCACGCCCTCCGT 720
b GCGGCACCTCACCCCTCTCGTTACCGTCGGCTCTGGTGTCTGGTGCAGGGCA
A V E W E S N G Q P E N N Y K T T P P V -
721 GCTGGACTCCGACGGCTCCTCTTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTG 780
b CGACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTGAGTGGCACCTGTTCTCGTCCAC
L D S D G S F F L Y S K L T V D K S R W -
781 GCAGCAGGGAACGTCTTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACAC 840
b CGTCGTCCCTTGCAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGTG
Q Q G N V F S C S V M H E A L H N H Y T -
841 GCAGAAGAGCCTCTCCCTGCTCCGGTAAATAATGGATCC 881
b CGTCTTCTCGGAGAGGGACAGAGGCCATTATTACCTAGG
Q K S L S L S P G K *

FIG. 16

XbaI

1 TCTAGATTGTTAACTAATTAAAGGAGGAATAACATATGGACAAAACACACATGTC
1 AGATCTAAACAAAATTGATTAATTCTCTCTTATTGTATACCTGTTTGAGTGTGTACAG
c M D K T H T C P .
61 CACCTTGCAGCACCTGAACCTGGGGGACCGTCAGTTCTCTCCAAAAAC
61 GTGGAACGGGTCTGGACTTGAGGACCCCCCTGGCAGTCAAAAGAGAAGGGGGTTTG
c P C P T A P E L L G G P S V F L F P P K P .
121 CCAAGGACACCCCTCATGATCTCCGGACCCCTGAGGTACATGGTGGTGGACGTGA
121 GGTTCTGTGGAGTACTAGAGGGCTGGGACTCCAGTGTACGCCACCCACTGCACT
c K D T L M I S R T P E V T C V V V D V S .
181 GCCACGAAGACCCCTGAGGTCAAGTTCAACTGGTACGTGGACGGGTGCATAATG
181 CGGTGCTCTGGACTCCAGTTCAAGTTGACCATGCACCTGCCACCTCACGTATTAC
c H E D P E V K F N W Y V D G V E V H N A .
241 CCAAGACAAAGCCGGAGGAGCAGTACAACACGTACCGTGTGGTACCGTCTCA
241 GGTTCTGTGGCTCCCTCGTATGTTGTCATGGCACACCCAGTCGAGGAGT
c K T K P R E E Q Y N S T Y R V V S V L T .
301 CCGTCCTGCACCAGGACTGGCTGAATGCAAGGAGTACAAGTGCAGGTCTCCAACAAAG
301 GGCAGGACGTGGCTCTGACCGACTTACCGTCTCATGTTCACGTTCCAGAGGTTGTTTC
c V L H Q D W L N G K E Y K C K V S N K A .
361 CCCTCCCAGCCCCATCGAGAAAACCATCTCAAAGCAAAGGGCAGCCCGAGAACAC
361 GGGAGGGTCGGGGTAGCTTTGGTAGAGGTTTGGTCCGGCTCTGGT
c L P A P I E K T I S K A K G Q P R E P . Q .
421 AGGTGTACACCCCTGCCTCCATCCGGATGAGCTGACCAAGAACAGGTACGCTGACCT
421 TCCACATGTGGGACGGAGGTAGGGCCCTACTCGACTGGTCTTGGTCCAGTCGGACTGGA
c V Y T L P P S R D E L T K N Q V S L T C .
481 GCCTGGTCAAAGGTTCTATCCCAGCGACATGCCGTGGAGTGGAGAGCAATGGCAGC
481 CGGACCAAGTTCCGAAGATAGGGTCGCTGTAGCGGCACCTCACCCCTCGTTACCGTCG
c L V K G F Y P S D I A V E W E S N G Q P .
541 CGGAGAACAACTACAAGACCAACGCCCTCCGTGGACTCCGACGGCTCCCTCTCT
541 GCCTCTTGTGATGTTCTGGCGGGACGACCTGAGGCTGCCAGGAAGAAGGAGA
c E N N Y K T T P P V L D S D G S F F L Y .
601 ACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGAACGTCTCTCATGCTCCG
601 TGTCTGTTGAGTGGCACCTGTTCTCGTCCACCGTCTGAGAACAGACTGAGGC
c S K L T V D K S R W Q Q G N V F S C S V .
661 TGATGCATGAGGCTCTGCACAACCACTACACGAGAAGAGCCTCTCCCTGCTCCGGTA
661 ACTACGTACTCCGAGACGTGTTGGTAGTGTGCGTCTCTCGGAGAGGGACAGAGGCCAT
c M H E A L H N H Y T Q K S L S L S P G K .
721 AAGGTGGAGGTGGCGGGAGGTACTTACTCTTGCACCTCGGCCACTGACTGGTTT
721 TTCCACCTCCACCGCCCTCATGAATGAGAACGGTGAAGCCGGTGACTGAACCCAAA
c G G G G G G G T Y S C H F G P L T W V C .
781 GCAAACCGCAGGGTGGCGGGCGGGCGGGTACCTATTCTGTCAATTGGCCCGC
781 CGTTTGGCGTCCCACCGCCGCCGCCACCATGGATAAGGACAGTAAACCGGGCG
c K P Q G G G G G G G G T Y S C H F G P L .
841 TGACCTGGGTATGTAAGCCACAAGGGGTTAACATCGAGGATCC
841 ACTGGACCCATACATTGGTGTCCCCAATTAGAGCTCTAGG
c T W V C K P Q G G * 884

FIG. 17A

[AatII sticky end]
(position #4358 in pAMG21)

5' GCGTAACGTATGCATGGTCTCC -
3' TGCACGCATTGCATACTGAGTACAGAGG -

- CCATGCGAGAGTAGGAACTGCCAGGCATCAAATAAAACGAAAGGCTAGTCGAAAGACT -
- GGTACGCTCTCATCCCTGACGGTCCGTAGTTATTTGCTTCCGAGTCAGCTTCTGA -
- GGGCCTTCGTTTATCTGTTGTTGCGGTGAACGCTCTCCTGAGTAGGACAAATCCGC -
- CCCGGAAAGCAAAATAGACAACAAACAGCCACTTGCAGAGGACTCATCCTGTTAGGCG -
- CGGGAGCGGATTGAAACGTTGCGAAGCAACGGCCGGAGGGTGGCGGGCAGGACGCCGC -
- GCCCTCGCCTAAACTGCAACGCTTCGTTGCCGGCCTCCCACCGCCCTGCGGGCG -
- CATAAACTGCCAGGCATCAAATTAGCAGAAGGCCATCCTGACGGATGGCTTTGCGT -
- GTATTTGACGGTCCGTAGTTAATTGCTTCCGGTAGGACTGCCTACCGGAAAAACGCA -

AatII

- TTCTACAAACTCTTTGTTATTTCTAAATACATTCAAATATGGACGTCGTACTTAAC -
- AAGATGTTGAGAAAACAAATAAAAGATTATGTAAGTTATACCTGCAGCATGAATTG -
- TTTAAAGTATGGCAATCAATTGCTCCTGTTAAAATTGCTTAGAAATACTTGGCAGC -
- AAAATTCTACACCGTTAGTTAACGAGGACAATTAAACGAAATCTTATGAAACCGTCG -
- GGTTTGTGTATTGAGTTCAATTGCGCATTGGTTAAATGGAAAGTGACCGTGCCTTAC -
- CCAAACAAACATAACTCAAAGTAAACCGTAACCAATTACCTTCACTGGCACCGGAATG -
- TACAGCCTAATATTTGAAATATCCAAGAGCTTTCTCGCATGCCACGCTAAAC -
- ATGTCGGATTATAAAACTTTAGGGTCTCGAAAAAGGAAGCGTACGGTGCCTTAC -
- ATTCTTTCTCTTTGGTTAAATGTTGATTATTGCTATATTATTTTC -
- TAAGAAAAAGAGAAAACCAATTAGCAACAAACTAAATAAACGATATAAAATAAAAG -
- GATAATTATCAACTAGAGAAGGAACAATTAGGTATGTCATACACGCATGAAAAATA -
- CTATTAATAGTTGATCTCTCCTGTTAATTACCATACAAGTATGTCGTACATTTCAT -
- AACTATCTATATAGTTGCTTCTCTGAATGTGCAAAACTAACGATTCCGAAGCCATTAT -
- TTGATAGATATCAACAGAAAGAGACTTACACGTTGATTGCTAAGGCTTCGGTAATA -
- TAGCAGTATGAATAGGGAAACTAAACCCAGTGATAAGACCTGATGATTCGCTTCTTAA -
- ATCGTCATACTTATCCCTTGATTGGTCACTATTCTGGACTAAAGCGAAGAAATT -
- TTACATTGGAGATTTTATTTACAGCATGTTCAAATATATTCAATTATCGGTG -
- AATGTAACCTCTAAAAATAATGTCGTACAAAAGTTATATAAGGTTAATTAGCCAC -
- AATGATTGGAGTTAGAATAATCTACTATAGGATCATTTTATTAAATTAGCGTCATCAT -
- TTACTAACCTCAATCTTATTAGATGATCTTAGTATAAAATAATTAAATCGCAGTAGTA -
- AATATTGCCCTCATTAGGGTAATTATCCAGAATTGAAATATCAGATTAAACCATAAG -
- TTATAACGGAGGTAAAAATCCCATTAAATAGGTCTTAACCTTATAGTCTAAATTGGTATC -
- AATGAGGATAAAATGATCGCGAGTAAATAATATTACAATGTACCATTAGTCATATCAG -
- TTACTCCTATTACTAGCGCTCATTTATTATAAGTGTACATGGTAAATCAGTATAGTC -
- ATAAGCATTGATTAATATCATATTGCTTCTACAGGCTTAAATTATTAAATTCTGT -
- TATTGCTAACTAATTATAGTAATAACGAAGATGTCCGAAATTAAATAATTAAAGACA -
- AAGTGTGTCGGCATTATGTCTTCATACCCATCTCTTATCCTTACCTATTGTTGTC -
- TTCACAGCAGCCGTAAATACAGAAAGTATGGTAGAGAAATAGGAATGGATAACAAACAG -
- GCAAGTTTGCCTGTTATATCATTAAAACGGTAATAGATTGACATTGATTCTAATAA -
- CGTTCAAAACGCACAATATAGTAATTGCCATTATCTAACTGTAAACTAAGATTATT -

FIG. 17B

- ATTGGATTTTCACACTATTATCGCTTCAAATACAATTGTTAACATAAGTACCTG -
- TAACCTAAAAACAGTGTGATAATATAGCGAACTTATGTTAACAAATTGTATTGAC -
- TAGGATCGTACAGGTTACGCAAGAAAATGGTTGTTAGTCGATTAATCGATTGATT -
- ATCCTAGCATGTCCAAATGCGTTCTTACCAAACAATATCAGCTAATTAGCTAAACTAA -
- CTAGATTGTTAACTAATTAAAGGAGGAATAACATATGGTTAACGCGTTGGAATTGCA -
- GATCTAAACAAAATTGATTAATTCCCTCCTATTGTATACCAATTGCGAACCTTAAGCT -

SacII
- GCTCACTAGTGTGACCTGCAGGGTACCATGGAAGCTTACTCGAGGGATCCGCGAAAGAA -
- CGAGTGATCACAGCTGGACGTCCCAGGTACCTTCGAATGAGCTCCTAGGCGCCTTCTT -
- GAAGAAGAAGAAGAAAGCCGAAAGGAAGCTGAGTTGGCTGCTGCCACCGCTGAGCAATA -
- CTTCTTCTTCTTCTTCGGGCTTCCTCGACTCAACCGACGACGGTGGCGACTCGTTAT -
- ACTAGCATAACCCCTGGGGCCTCTAAACGGTCTTGAGGGTTTGCTGAAAGGAGG -
- TGATCGTATTGGGGAACCCCGGAGATTGCCAGAACTCCCCAAAAACGACTTCCTCC -
- AACCGCTCTCACGCTTACGC 3' [SacII sticky end]
- TTGGCGAGAAGTGCAGAGAAGTG 5' (position #5904 in pAMG21)

FIG.18A - 1

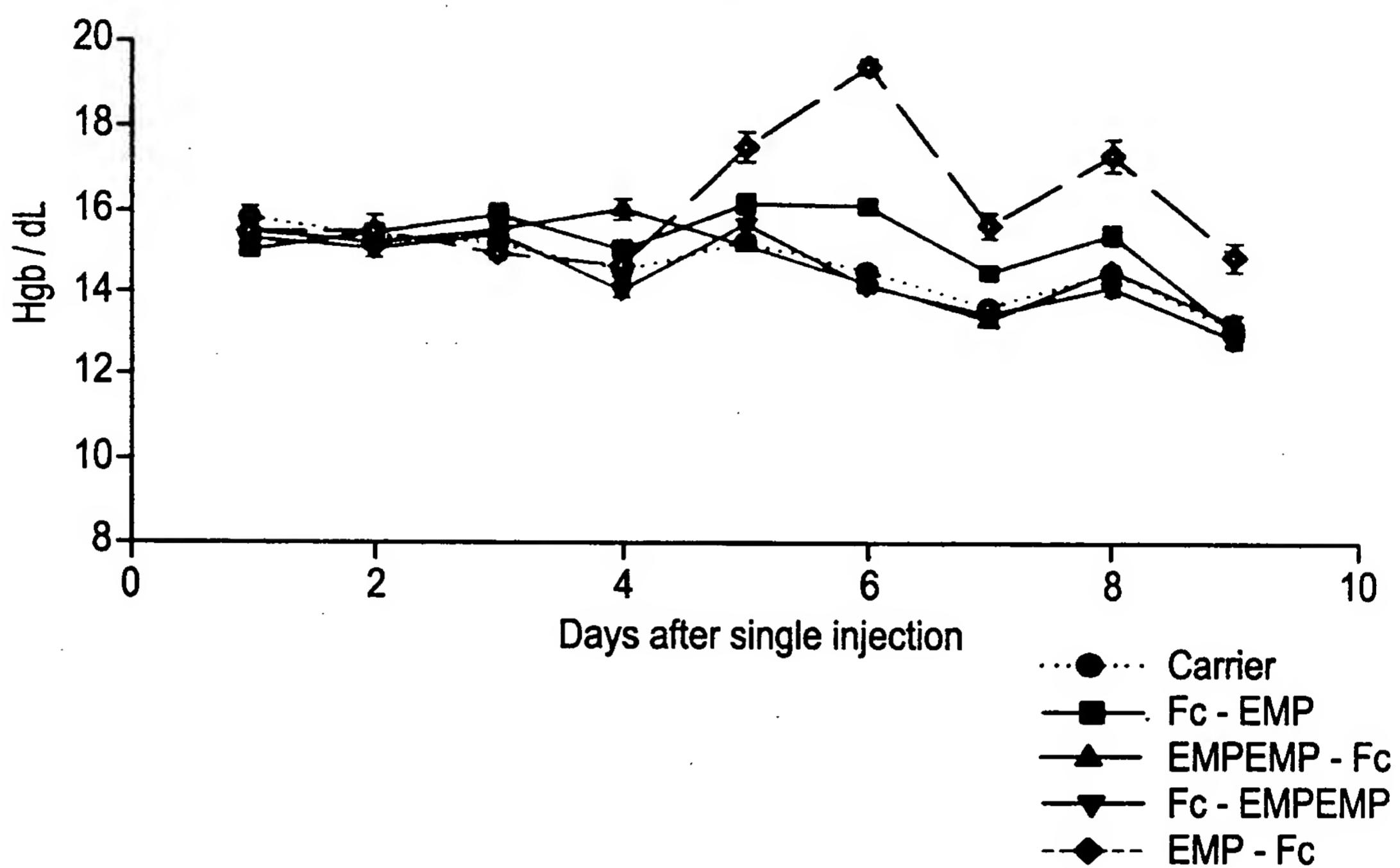


FIG.18A - 2

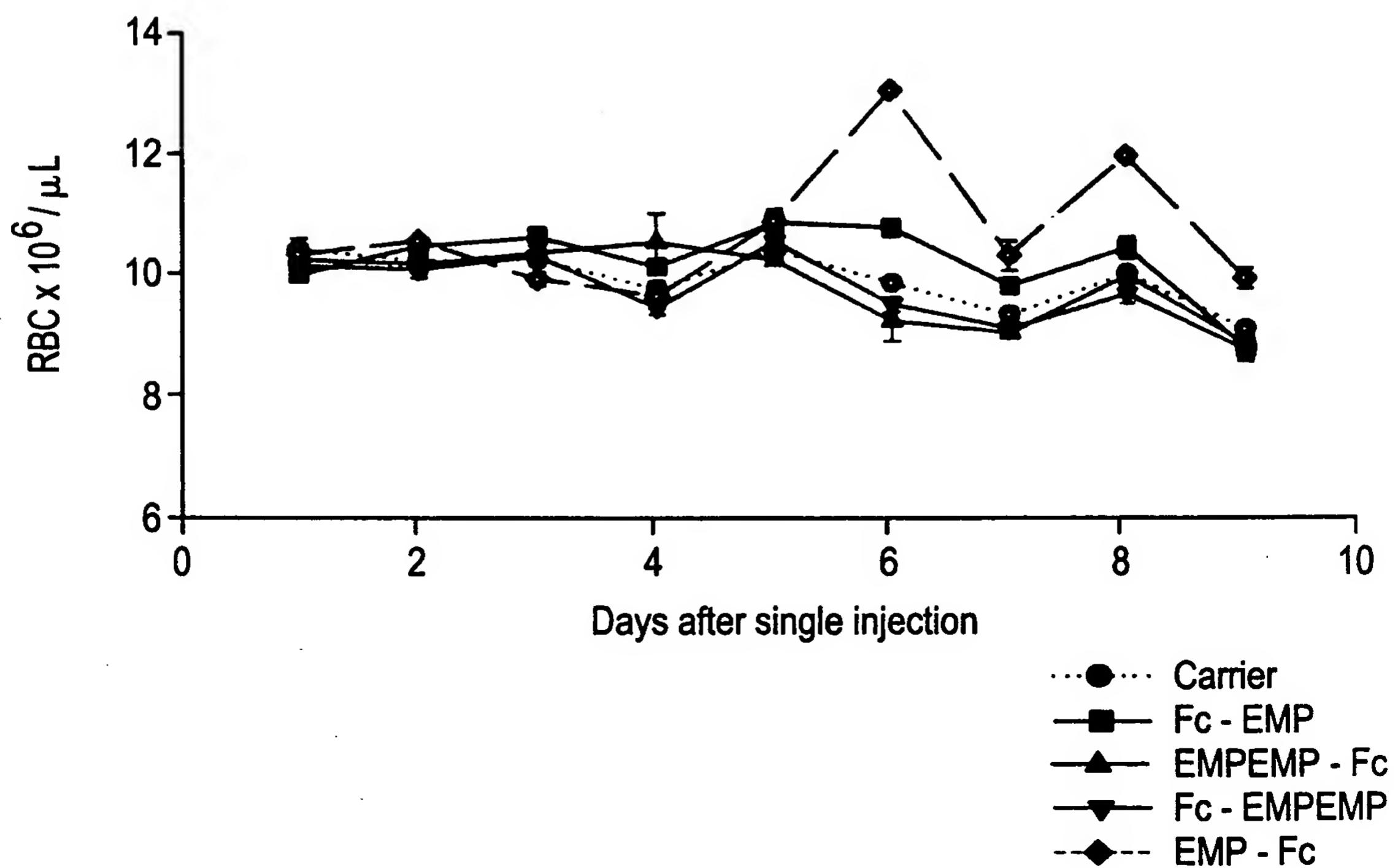


FIG.18A - 3

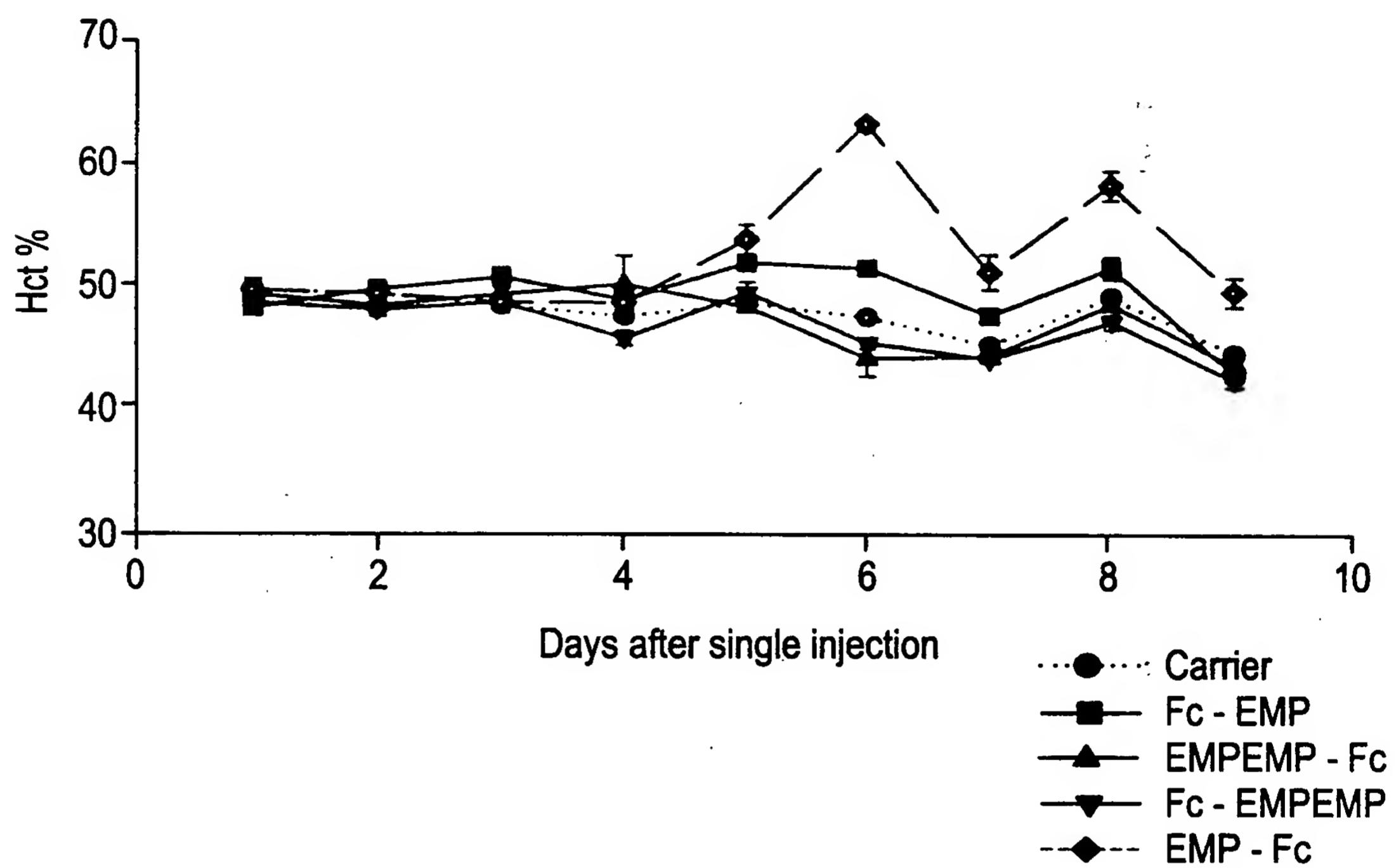


FIG.18B - 1

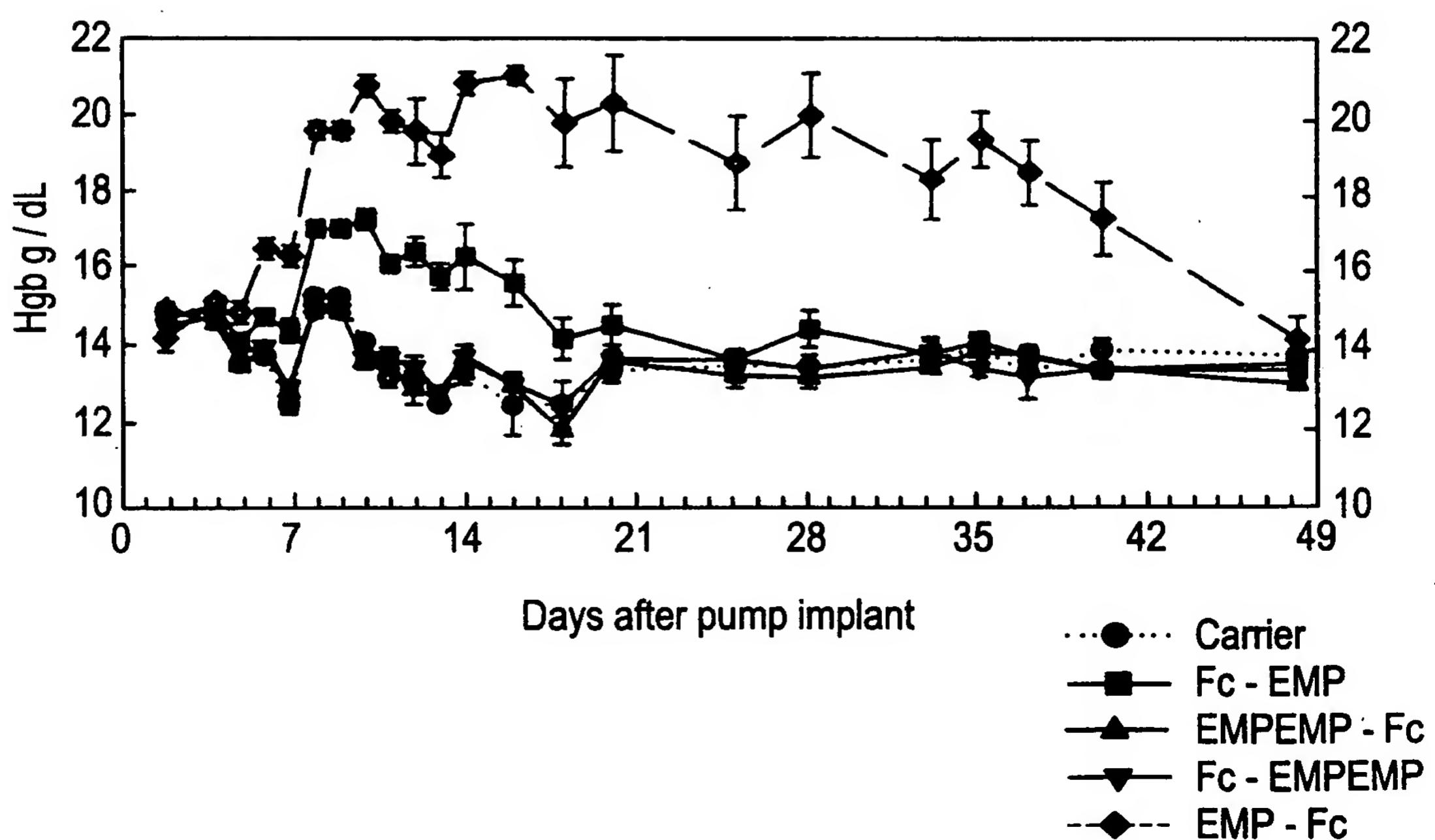


FIG.18B - 2

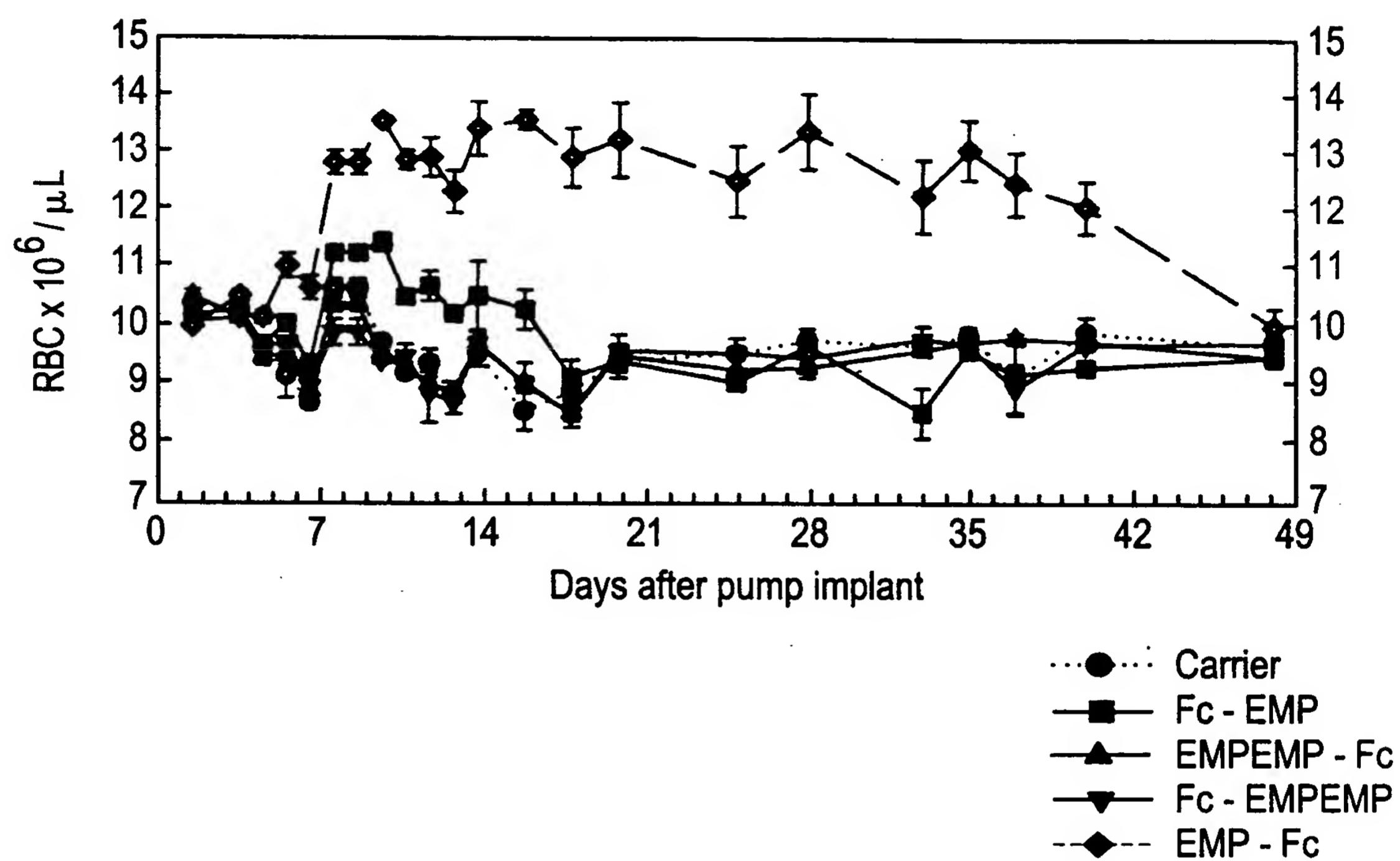


FIG.18B - 3

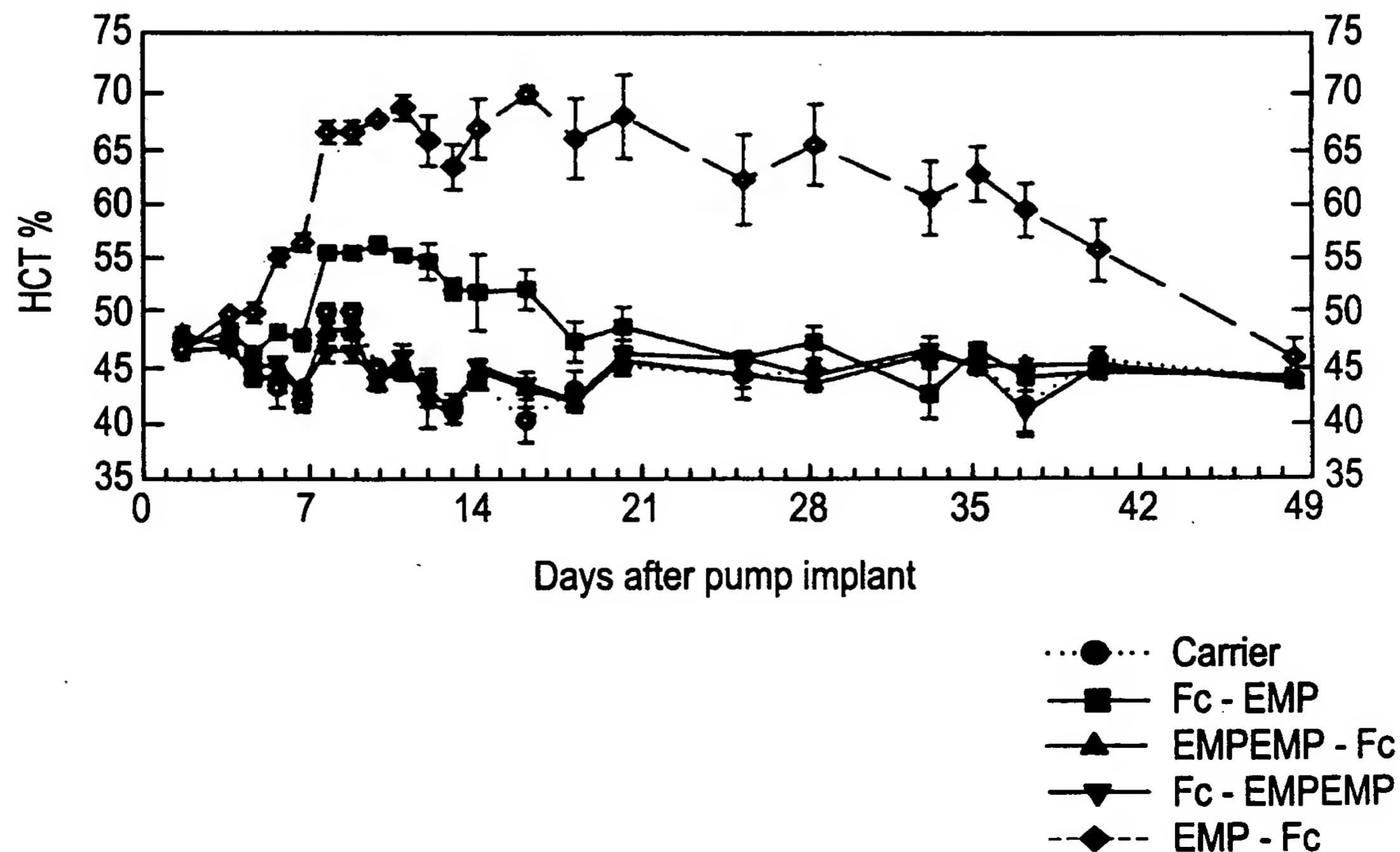


FIG. 19A

NdeI |

1 CATATGGACAAAACACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGACCG 60
1 GTATACTGTTGAGTGTACAGGTGGAACAGGTCGAGGCCTGAGGACCCCCCTGGC

a M D K T H T C P P C P A P E L L G G P -
61 TCAGTCTCCTCTTCCCCAAAACCCAAAGGACACCCCTCATGATCTCCGGACCCCTGAG 120
61 AGTCAGAAGGAGAAGGGGGTTTGGGTTCTGTGGGAGTACTAGAGGGCTGGGACTC

a S V F L F P P K P K D T L M I S R T P E -
121 GTCACATGCGTGGTGGACGTGAGCCACGAAGACCCCTGAGGTCAAGTTCAACTGGTAC 180
121 CAGTGTACGCACCACCTGCACTCGGTGCTCTGGACTCCAGTTCAAGTTGACCATG

a V T C V V V D V S H E D P E V K F N W Y -
181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240
181 CACCTGCCGCACCTCCACGTATTACGGTTCTGTTGGCGCCCTCGTCATGTTGTCG

a V D G V E V H N A K T K P R E E Q Y N S -
241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCTGCACCAAGGACTGGCTGAATGGCAAGGAG 300
241 TGCATGGCACACCAGTCGAGGAGTGGCAGGACGTGGCCTGACCGACTTACCGTTCTC

a T Y R V V S V L T V L H Q D W L N G K E -
301 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCAGCCCCCATCGAGAAAACCATCTCCAAA 360
301 ATGTTACGTTCCAGAGGTTGTTGGGAGGGTCGGGGTAGCTTTGGTAGAGGTTT

a Y K C K V S N K A L P A P I E K T I S K -
361 GCCAAAGGGCAGCCCCGAGAACACAGGTGTACACCCCTGCCCATCCGGATGAGCTG 420
361 CGGTTCCCGTCGGGCTCTGGTGTCCACATGTGGACGGGGTAGGGCCCTACTCGAC

a A K G Q P R E P Q V Y T L P P S R D E L -
421 ACCAAGAACCAAGGTAGCCTGACCTGCCTGGTCAAAGGCTCTATCCAGCGACATGCC 480
421 TGGTTCTGGTCCAGTCGGACTGGACGGACCAGTTCCGAAGATAGGGTCGCTGTAGCGG

a T K N Q V S L T C L V K G F Y P S D I A -
481 GTGGAGTGGAGAGCAATGGCAGCCGGAGAACAACTACAAGACCACGCCCTCCGTGCTG 540
481 CACCTCACCCCTCTCGTTACCCGTCGGCCTCTGTTGATGTTCTGGTGGAGGGCACGAC

a V E W E S N G Q P E N N Y K T T P P V L -
541 GACTCCGACGGCTCCTTCTTCTACAGCAAGCTACCGTGGACAAGAGCAGGTGGCAG 600
541 CTGAGGCTGCCAGGAAGAAGGAGATGTCGTTGAGTGGCACCTGTTCTCGTCCACCGTC

a D S D G S F F L Y S K L T V D K S R W Q -

FIG. 19B

CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG
601 -----+-----+-----+-----+-----+-----+-----+-----+ 660
GTCCCCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTATGTGCGTC

a Q G N V F S C S V M H E A L H N H Y T Q -

AAGAGCCTCTCCCTGTCTCCGGTAAAGGTGGAGGTGGTGGTACTTCCTGCCGCACTAC
661 -----+-----+-----+-----+-----+-----+-----+-----+ 720
TTCTCGGAGAGGGACAGAGGCCATTCCACCTCCACCACCACTGAAGGACGGCGTGATG

a K S L S L S P G K G G G G G D F L P H Y -

BamHI:
|
721 AAAAAACACCTCTGGGTACCGTCCGTAATGGATCC 757
TTTTGTGGAGAGACCCAGTGGCAGGCATTACCTAGG

a K N T S L G H R P *

FIG. 20A

NdeI
|
1 CATATGGACTTCCTGCCGCACTACAAAAACACCTCTGGGTACCGTCCGGTGGAGGC 60
1 GTATACTGAAGGACGGCGTGATGTTTGTGGAGAGACCCAGTGGCAGGCCACCTCCG
a M D F L P H Y K N T S L G H R P G G G -
61 GGTGGGGACAAAACCTCACACATGTCCACCTGCCAGCACCTGAACCTGGGGGACCG 120
61 CCACCCCTGTTTGAGTGTACAGGTGGAACGGTCGTGGACTTGAGGACCCCCCTGGC
a G G D K T H T C P P C P A P E L L G G P -
121 TCAGTTTCCTCTTCCCCAAAACCAAGGACACCTCATGATCTCCGGACCCCTGAG 180
121 AGTAAAAGGAGAAGGGGGTTTGGGTTCTGTGGAGTACTAGAGGCCTGGGACTC
a S V F L F P P K P K D T L M I S R T P E -
181 GTCACATGCGTGGTGGACGTGAGCCACGAAGACCCCTGAGGTCAAAGTTCAACTGGTAC 240
181 CAGTGTACGCACCACCTGCACTCGGTGCTCTGGACTCCAGTTCAAGTTGACCATG
a V T C V V V D V S H E D P E V K F N W Y -
241 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGGGAGGAGCAGTACAACAGC 300
241 CACCTGCCGCACCTCACGTATTACGGTTCTGTTGGCGCCCTCGTCATGTTGTCG
a V D G V E V H N A K T K P R E E Q Y N S -
301 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAAGGACTGGCTGAATGGCAAGGAG 360
301 TGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGCCTGACCGACTTACCGTTCTC
a T Y R V V S V L T V L H Q D W L N G K E -
361 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCAGCCCCATCGAGAAAACCATCTCCAAA 420
361 ATGTTCACGTTCCAGAGGTTGTTGGGAGGGTCGGGGTAGCTTTGGTAGAGGTTT
a Y K C K V S N K A L P A P I E K T I S K -
421 GCCAAAGGGCAGCCCCGAGAACACAGGTGTACACCCCTGCCCATCCGGATGAGCTG 480
421 CGGTTCCCGTCGGGCTCTGGTGTCCACATGTGGACGGGGTAGGGCCCTACTCGAC
a A K G Q P R E P Q V Y T L P P S R D E L -
481 ACCAAGAACCGAGTCAGCCTGACCTGCCCTGGTCAAAGGCTTCTATCCCAGCGACATGCC 540
481 TGGTTCTGGTCCAGTCGGACTGGACGGACCAGTTCCGAAGATAGGGCGCTGTAGCGG
a T K N Q V S L T C L V K G F Y P S D I A -
541 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCAAGCCTCCGTGCTG 600
541 CACCTCACCCCTCTCGTTACCCGTGGCCTCTGTTGATGTTCTGGTGGAGGGCACGAC
a V E W E S N G Q P E N N Y K T T P P V L -

FIG. 20B

601 GACTCCGACGGCTCCTCTTCTACAGCAAGCTACCGTGGACAAGAGCAGGTGGCAG 660
-----+-----+-----+-----+-----+-----+-----+-----+
CTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTC

a D S D G S F F L Y S K L T V D K S R W Q -

661 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 720
-----+-----+-----+-----+-----+-----+-----+-----+
GTCCCCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTATGTGCGTC

a Q G N V F S C S V M H E A L H N H Y T Q -

BamHI
|
721 AAGAGCCTCTCCCTGTCTCCGGTAAATAATGGATCCGCGG 761
-----+-----+-----+-----+
TTCTCGGAGAGGGACAGAGGCCATTATTACCTAGGCGCC

a K S L S L S P G K *

FIG. 21A

NdeI

1 CATATGGACAAAACACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGACCG 60
1 GTATACTGTTTGAGTGTACAGGTGGAACAGGTGAGGGCTTGAGGACCCCCCTGGC

a M D K T H T C P P C P A P E L L G G P -

61 TCAGTCTCCTCTTCCCCAAAACCAAGGACACCCCTCATGATCTCCGGACCCCTGAG 120
61 AGTCAGAAGGAGAAGGGGGTTTGGGTTCTGTGGGAGTACTAGAGGGCTGGGACTC

a S V F L F P P K P K D T L M I S R T P E -

121 GTCACATGCGTGGTGGACGTGAGCCACGAAGACCCCTGAGGTCAAGTTCAACTGGTAC 180
121 CAGTGTACGCACCACCTGCACCGTGCCTGGACTCCAGTTCAAGTTGACCATG

a V T C V V V D V S H E D P E V K F N W Y -

181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGGAGGAGCAGTACAACAGC 240
181 CACCTGCCGCACCTCCACGTATTACGGTTCTGGCGCCCTCCTCGTCATGTTGTCG

a V D G V E V H N A K T K P R E E Q Y N S -

241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG 300
241 TGCATGGCACACCAGTCGAGGACTGGCAGGACGTGGCCTGACCGACTTACCGTTCTC

a T Y R V V S V L T V L H Q D W L N G K E -

301 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCAGCCCCATCGAGAAAACCATCTCCAAA 360
301 ATGTTACGTTCCAGAGGTTGTTGGAGGGTAGCTTTGGTAGAGGTT

a Y K C K V S N K A L P A P I E K T I S K -

361 GCCAAAGGGCAGCCCCGAGAACACAGGTGTACACCCCTGCCCATCCGGATGAGCTG 420
361 CGGTTCCCGTCGGGCTTGGTGTCCACATGTGGGACGGGGTAGGGCCCTACTCGAC

a A K G Q P R E P Q V Y T L P P S R D E L -

421 ACCAAGAACCAAGGTAGCCTGACCTGCCTGGTCAAAGGCTCTATCCCAGCGACATGCC 480
421 TGGTTCTGGTCCAGTCGGACTGGACGGACCAGTTCCGAAGATAGGGTCGCTGTAGCGG

a T K N Q V S L T C L V K G F Y P S D I A -

481 GTGGAGTGGAGAGCAATGGCAGCCGGAGAACAACTACAAGACCAAGCCTCCGTGCTG 540
481 CACCTCACCCCTCGTTACCGTCGGCCTCTGTTGATGTTCTGGTGCAGGGCACGAC

a V E W E S N G Q P E N N Y K T T P P V L -

541 GACTCCGACGGCTCCTCTTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600
541 CTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTGAGTGGCACCTGTTCTCGTCCACCGTC

a D S D G S F F L Y S K L T V D K S R W Q -

FIG. 21B

601 CAGGGGAACGTCTTCTATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG
660 GTCCCCCTTGCAGAAGAGTACGAGGCACCTACGTACTCCGAGACGTGTTGGTATGTGCGTC

a Q G N V F S C S V M H E A L H N H Y T Q -

661 AAGAGCCTCTCCCTGTCTCCGGTAAAGGTGGAGGTGGTGGTTCGAATGGACCCGGGT
720 TTCTCGGAGAGGGACAGAGGCCATTCCACCTCCACCACCAAAGCTTACCTGGGGCCA

a K S L S L S P G K G G G G G F E W T P G -

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721 TACTGGCAGCCGTACGCTCTGCCGCTGTAATGGATCCCTCGAG
763 ATGACCGTCGGCATGCGAGACGGCGACATTACCTAGGGAGCTC

a Y W Q P Y A L P L *

FIG. 22A

NdeI

1 CATATGTTCGAATGGACCCGGTTACTGGCAGCCGTACGCTCTGCCGCTGGGTGGAGGC
1 GTATAACAAGCTTACCTGGGGCCAATGACCGTCGGCATGCGAGACGGCGACCCACCTCCG 60

a M F E W T P G Y W Q P Y A L P L G G G -

61 GGTGGGGACAAAACACACATGTCCACCTTGCCTGGCAGCACCTGAACCTGGGGGGACCG
61 CCACCCCTGTTTGAGTGTACAGGTGGAACGGGTGCTGGACTTGAGGACCCCCCTGGC 120

a G G D K T H T C P P C P A P E L L G G P -

121 TCAGTTTCCTCTTCCCCAAAACCCAAGGACACCCCTCATGATCTCCGGACCCCTGAG
121 AGTAAAAGGAGAAGGGGGTTTGGGTTCTGTGGAGTACTAGAGGCCTGGGACTC 180

a S V F L F P P K P K D T L M I S R T P E -

181 GTCACATGCGTGGTGGGACGTGAGCCACGAAGACCCCTGAGGTCAAGTTCAACTGGTAC
181 CAGTGTACGCACCACCTGCACTCGGTGCTCTGGACTCCAGTTCAAGTTGACCATG 240

a V T C V V V D V S H E D P E V K F N W Y -

241 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGGAGGAGCAGTACAACAGC
241 CACCTGCCGCACCTCCACGTATTACGGTTCTGTTGGCGCCCTCCTCGTCATGTTGTCG 300

a V D G V E V H N A K T K P R E E Q Y N S -

301 ACGTACCGTGTGGTCAGCGTCTCACCGTCTGCACCAAGGACTGGCTGAATGGCAAGGAG
301 TGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGCCTGACCGACTTACCGTCTC 360

a T Y R V V S V L T V L H Q D W L N G K E -

361 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCAGCCCCATCGAGAAAACATCTCCAAA
361 ATGTTCACGTTCCAGAGGTTGTTGGGAGGGTAGCTTTGGTAGAGGTTT 420

a Y K C K V S N K A L P A P I E K T I S K -

421 GCCAAAGGGAGCCCCGAGAACACAGGTGTACACCCCTGCCCATCCGGATGAGCTG
421 CGGTTTCCCCTGTCGGGCTCTGGTGTCCACATGTGGGACGGGGTAGGGCCCTACTCGAC 480

a A K G Q P R E P Q V Y T L P P S R D E L -

481 ACCAAGAACCAAGGTCAAGCTGACCTGCCTGGTCAAAGGCTCTATCCAGCGACATGCC
481 TGGTTCTGGTCCAGTCGGACTGGACGGACCAGTTCCGAAGATAGGGTCGCTGTAGCGG 540

a T K N Q V S L T C L V K G F Y P S D I A -

541 GTGGAGTGGAGAGCAATGGCAGCCGGAGAACAAACTACAAGACCAACGCCCTCCGTGCTG
541 CACCTCACCCCTCTCGTTACCGTCGGCCTCTGTTGATGTTCTGGTGCAGGGCACGAC 600

a V E W E S N G Q P E N N Y K T T P P V L -

FIG. 22B

601 GACTCCGACGGCTCCTTCTTCTACAGCAAGCTACCGTGGACAAGAGCAGGTGGCAG
660 CTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTGAGTGGCACCTGTTCTCGTCCACCGTC
a D S D G S F F L Y S K L T V D K S R W Q -
661 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG
720 GTCCCCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTATGTGCGTC
a Q G N V F S C S V M H E A L H N H Y T Q -
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721 AAGAGCCTCTCCCTGTCTCCGGTAAATAATGGATCC
757 TTCTCGGAGAGGGACAGAGGCCATTATTACCTAGG
a K S L S L S P G K *

FIG. 23A

NdeI

1 CATATGGACAAAACACACATGTCCACCGTGCCAGCACCTGAACCTGGGGGACCG
1 GTATAACCTGTTTGAGTGTACAGGTGGCACGGTCGTGGACTTGAGGACCCCCCTGGC 60

a M D K T H T C P P C P A P E L L G G P -

61 TCAGTTTCCTCTTCCCCAAAACCAAGGACACCCCTCATGATCTCCGGACCCCTGAG
61 AGTAAAAGGAGAAGGGGGTTTGGGTTCTGTGGAGTACTAGAGGGCTGGGACTC 120

a S V F L F P P K P K D T L M I S R T P E -

121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCCTGAGGTCAAGTTCAACTGGTAC
121 CAGTGTACGCACCACCTGCACACTCGTGCTCTGGACTCCAGTTCAAGTTGACCATG 180

a V T C V V V D V S H E D P E V K F N W Y -

181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGGAGGAGCAGTACAACAGC
181 CACCTGCCGCACCTCCACGTATTACGGTTCTGGCGCCCTCGTCATGTTGTCG 240

a V D G V E V H N A K T K P R E E Q Y N S -

241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAAGGACTGGCTGAATGGCAAGGAG
241 TGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGCCTGACCGACTTACCGTCCTC 300

a T Y R V V S V L T V L H Q D W L N G K E -

301 TACAAGTGCAGGTCTCCAACAAAGCCCTCCCAGCCCCATCGAGAAAACATCTCCAAA
301 ATGTTCACGTTCCAGAGGTTGTTGGAGGGTAGCTTTGGTAGAGGTTT 360

a Y K C K V S N K A L P A P I E K T I S K -

361 GCCAAAGGGCAGCCCCGAGAACACAGGTGTACACCCCTGCCCGGATGAGCTG
361 CGGTTCCCGTCGGGCTCTGGTGTCCACATGTGGGACGGGGTAGGGCCCTACTCGAC 420

a A K G Q P R E P Q V Y T L P P S R D E L -

421 ACCAAGAACCAAGGTCAGCCTGACCTGCCTGGTCAAAGGCTCTATCCCAGCGACATGCC
421 TGGTTCTGGTCCAGTCGGACTGGACGGACCAGTTCCGAAGATAGGGCGCTGTAGCGG 480

a T K N Q V S L T C L V K G F Y P S D I A -

481 GTGGAGTGGAGAGCAATGGCAGCCGGAGAACAACTACAAGACCAACGCCCTCCGTGCTG
481 CACCTCACCCCTCGTTACCGTCGGCCTCTGTTGATGTTCTGGTGCAGGGCACGAC 540

a V E W E S N G Q P E N N Y K T T P P V L -

541 GACTCCGACGGCTCCTCTTCTACAGCAAGCTACCGTGGACAAGAGCAGGTGGCAG
541 CTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTGAGTGGCACCTGTTCTCGTCCACCGTC 600

a D S D G S F F L Y S K L T V D K S R W Q -

FIG. 23B

601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG
660 GTCCCCCTTGCAGAAGAGTACGAGGCACACTACGTACTCCGAGACGTGTTGGTGTGCGTC

a Q G N V F S C S V M H E A L H N H Y T Q -

661 AAGAGCCTCTCCCTGTCTCCGGTAAAGGTGGTGGTGGTGGTGAACCGAACTGTGAC
720 TTCTCGGAGAGGGACAGAGGCCATTCCACCACCACCAACTGGCTTGACACTG

a K S L S L S P G K G G G G G V E P N C D -

721 ATCCATGTTATGTGGGAATGGGAATGTTTGAACGTCTGTAACTCGAGGATCC
773 TAGGTACAATAACCCCTTACCCCTACAAAACTTGCAGACATTGAGCTCCTAGG

a I H V M W E W E C F E R L *

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FIG. 24A

FIG. 24B

601 CCTCCC GTGCTGGACTCCGACGGCTCCTCTTCCTCTACAGCAAGCTCACCGTGGACAAG
660 GGAGGGCACGACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTC
a P P V L D S D G S F F L Y S K L T V D K -
661 AGCAGGTGGCAGCAGGGAACGTCTTCTCATGCTCCGTATGCATGAGGCTCTGCACAAC
720 TCGTCCACCGT CGTCCCTTGAGAAGAGTACGAGGC ACTACGTACTCCGAGACGTGTTG
a S R W Q Q G N V F S C S V M H E A L H N -
721 CACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGTAAATAACTCGAGGATCC
773 GTGATGTGCGTCTCTCGGAGAGGGACAGAGGCCATTATTGAGCTCCTAGG
a H Y T Q K S L S L S P G K *

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FIG. 25A

NdeI
|
CATATGGACAAA
1 ACTCACACATGTCCACCTGTCCAGCTCCGGAACTCCTGGGGGACCG
60 GTATACTGTTTGAGTGTACAGGTGGAACAGGTCGAGGCCTTGAGGACCCCCCTGGC
a M D K T H T C P P C P A P E L L G G P -
61 TCAGTCTCCTCTTCCCCAAA
120 ACCAACCAAGGACACCCCTCATGATCTCCGGACCCCTGAG
AGTCAGAAGGAGAAGGGGGTTTGGGTTCTGTGGGAGTACTAGAGGCCTGGGACTC
a S V F L F P P K P K D T L M I S R T P E -
121 GTCACATGCGTGGTGGACGTGAGCCACGAAGACCCCTGAGGTCAAGTTCAACTGGTAC
180 CAGTGTACGCACCACCTGCACTCGGTGCTCTGGGACTCCAGTTCAAGTTGACCATG
a V T C V V V D V S H E D P E V K F N W Y -
181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGAGGAGCAGTACAACAGC
240 CACCTGCCGCACCTCCACGTATTACGGTTCTGTTGGCGCCCTCGTCATGTTGTCG
a V D G V E V H N A K T K P R E E Q Y N S -
241 ACGTACCGTGTGGTCAGCGTCCCTACCGTCTGCACCAAGGACTGGCTGAATGGCAAGGAG
300 TGCATGGCACACCAGTCGCAAGGTGGCAGGACGTGGCCTGACCGACTTACCGTTCC
a T Y R V V S V L T V L H Q D W L N G K E -
301 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCATCGAGAAAACCATCTCCAAA
360 ATGTTCACGTTCCAGAGGTTGTTGGGAGGGTCGGGGTAGCTTTGGTAGAGGTTT
a Y K C K V S N K A L P A P I E K T I S K -
361 GCCAAAGGGCAGCCCCGAGAACCAACAGGTGTACACCCCTGCCCATCCGGATGAGCTG
420 CGGTTCCCGTCGGGCTCTGGTGTCCACATGTGGGACGGGGTAGGGCCCTACTCGAC
a A K G Q P R E P Q V Y T L P P S R D E L -
421 ACCAAGAACCAAGGTCAACGCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC
480 TGGTTCTGGTCCAGTCGGACTGGACGGACCAGTTCCGAAGATAGGGTCGCTGTAGCGG
a T K N Q V S L T C L V K G F Y P S D I A -
481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCCTCCGTGCTG
540 CACCTCACCCCTCTCGTTACCGTCGGCCTCTGTTGATGTTCTGGTGGAGGGCACGAC
a V E W E S N G Q P E N N Y K T T P P V L -
541 GACTCCGACGGCTCCTTCTTCCCTACAGCAAGCTACCGTGGACAAGAGCAGGTGGCAG
600 CTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTGAGTGGCACCTGTTCTCGTCCACCGTC
a D S D G S F P L Y S K L T V D K S R W Q -

FIG. 25B

601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG
660
GTCCCCCTTGCAGAAGAGTACGAGGCACACTACGTACTCCGAGACGTGTTGGTATGTGCGTC

a Q G N V F S C S V M H E A L H N H Y T Q -

661 AAGAGCCTCTCCCTGTCTCCGGTAAAGGTGGAGGTGGTGGTGCACCACCCACTGGGT
720
TTCTCGGAGAGGGACAGAGGCCATTCCACCTCCACCAACGTGGTGGTGACCCCA

A K S L S L S P G K G G G G G C T T H W G -

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|
721 TTCACCCCTGTGCTAATGGATCCCTCGAG
748
AAGTGGGACACGATTACCTAGGGAGCTC

a F T L C *

FIG. 26A

NdeI

1 CATATGTGCACCACCCACTGGGGTTTACCCCTGTGCGGTGGAGGCGGTGGGGACAAAGGT
1 GTATACACGTGGTGGGTGACCCCAAAGTGGACACGCCACCTCCGCCACCCCTGTTCCA 60

a M C T T H W G F T L C G G G G G D K G -
61 GGAGGCGGTGGGGACAAAACACACATGTCCACCTGCCAGCACCTGAACCTCTGGGG
61 CCTCCGCCACCCCTGTTTGAGTGTACAGGTGGAACGGTCTGGACTTGAGGACCCC 120

a G G G G D K T H T C P P C P A P E L L G -
121 GGACCGTCAGTTCTCTTCCCCAAAACCCAAAGGACACCCCTCATGATCTCCGGACC
121 CCTGGCAGTCAAAAGGAGAAGGGGGTTTGGGTTCTGTGGAGTACTAGAGGGCTGG 180

a G P S V F L F P P K P K D T L M I S R T -
181 CCTGAGGTACATGCGTGGTGGACGTGAGCCACGAAGACCCCTGAGGTCAAGTTAAC
181 GGACTCCAGTGTACGCACCACCTGCACTCGGTCTGGACTCCAGTTCAAGTTG 240

a P E V T C V V V D V S H E D P E V K F N -
241 TGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGGGAGGAGCAGTAC
241 ACCATGCACCTGCCGCACCTCCACGTATTACGGTCTGGACTCCAGTTCAAGTTG 300

a W Y V D G V E V H N A K T K P R E E Q Y -
301 AACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCTGCACCAAGGACTGGCTGAATGGC
301 TTGTCGTGCATGGCACACCAGTCGCAAGTGGCAGGACGTGGCCTGACCGACTTACCG 360

a N S T Y R V V S V L T V L H Q D W L N G -
361 AAGGAGTACAAGTCAAGGTCTCCAACAAAGCCCTCCCAGCCCCATCGAGAAAACCATC
361 TTCCTCATGTTCACGTTCCAGAGGTTGTTGGGAGGGTCGGGGTAGCTCTTGGTAG 420

a K E Y K C K V S N K A L P A P I E K T I -
421 TCCAAAGCCAAGGGCAGCCCCGAGAACACAGGTGTACACCCCTGCCCATCCGGGAT
421 AGGTTTCGGTTCCCGTCGGGCTCTGGTGTCCACATGTGGGACGGGGTAGGGCCCTA 480

a S K A K G Q P R E P Q V Y T L P P S R D -
481 GAGCTGACCAAGAACCAAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGAC
481 CTCGACTGGTTCTGGTCCAGTCGGACTGGACGGACCAGTTCCGAAGATAGGGTCGCTG 540

a E L T K N Q V S L T C L V K G F Y P S D -
541 ATCGCCGTGGAGTGGGAGAGCAATGGCAGCCGGAGAACAACTACAAGACCACGCCCTCCC
541 TAGCGGCACCTCACCCCTCTCGTTACCCGTCGGCCTCTGGTGTGATGTTCTGGTGGAGGG 600

a I A V E W E S N G Q P E N N Y K T T P P -

FIG. 26B

601 GTGCTGGACTCCGACGGCTCCTCTTCTACAGCAAGCTCACCGTGGACAAGAGCAGG
660 CACGACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTGAGTGGCACCTGTTCTCGTCC
a V L D S D G S F F L Y S K L T V D K S R -
661 TGGCAGCAGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTAC
720 ACCGTCGTCCCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATG
a W Q Q G N V F S C S V M H E A L H N H Y -
721 ACGCAGAAGAGCCTCTCCCTGTCTCCGGTAAATAATGGATCC
763 TCGGTCTTCTCGGAGAGGGACAGAGGCCATTATTACCTAGG
a T Q K S L S L S P G K *

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